

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 15, 2004, 17:55:27 ; Search time 54 Seconds

(without alignments)  
2150.500 Million cell updates/sec

Title: US-09-980-350-2

Sequence: 1 MAPDLDPKSAQNSKPRLL.....LNGLTPHCAGEIAVENIK 411

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : A\_Geneseq\_29rand04:\*

1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2098	100.0	411	2	AAV34133 Human pot
2	2098	100.0	411	2	AAV28496
3	2098	100.0	411	4	AAV50044 Human TRE
4	2095	99.9	411	3	AAE10341 Human TRE
5	2087	99.5	411	5	AAE16597 Human TWI
6	2085	98.4	426	4	AAU07618 Human pot
7	2061	98.2	426	4	AAU07622 Human pot
8	2060	98.2	426	4	AAU07623 Human pot
9	2057	98.0	426	4	AAU07625 Human pot
10	2056	98.0	426	4	AAU07624 Human pot
11	2044	97.4	411	3	AAE10342
12	2038	97.1	411	2	AAV28497
13	1833	87.4	370	2	AAV30648
14	1641.5	78.2	337	6	AAE41487 Human DIT
15	1242.5	59.2	538	5	AAE47930 Human TRE
16	1242.5	59.2	538	5	AAE16596 Human TWI
17	1242.5	59.2	538	5	ABP69333 Human pol
18	1242.5	59.2	543	5	AAE21804 Human TRE
19	1242.5	59.2	543	5	AAU81354 Human hum
20	1242.5	59.2	543	5	AAU94742 Human nov
21	1242.5	59.2	543	5	ABE83542 Hypochala
22	1242.5	59.2	543	6	ADA05746 Human NOV
23	1242.5	59.2	543	7	ADE08315 Human pro
24	1238.5	59.0	543	5	AAU79473 Human nov
25	1215	57.9	724	5	AAO14193 Human tra

26	803	38.3	392	6	ABU60891	ABU60891 Human G p
27	803	38.3	393	3	AAV94426	Aay94426 Human h-t
28	803	38.3	393	3	AAV94425	Aay94425 Human h-t
29	803	38.3	393	4	AAV67777	AAV67777 Human mec
30	803	38.3	419	5	AAV78406	AAV78406 Amno aci
31	803	38.3	419	5	AAE38597	AAE38597 Human pot
32	803	38.3	1314	7	AAU04571	AAU04571 Human G-P
33	803	38.3	1314	6	ABU60872	ABU60872 Human G p
34	776.5	37.0	398	2	AAV30647	Aay30647 A mechan
35	768.5	36.6	398	5	AAE16598	AAE16598 Human TWI
36	635.5	30.3	383	4	ABG02731	ABG02731 Novel hum
37	578.5	27.6	421	4	ABE12229	ABE12229 Human K c
38	549	26.2	155	4	AAE21148	AAE21148 Human EST
39	549	26.2	155	7	AAE09289	AAE09289 Novel pro
40	547	26.1	107	2	AAV28498	AAV28498 Partial h
41	513	24.5	295	5	AAE21164	AAE21164 Human TRI
42	502.5	24.0	294	6	AAU99892	AAU99892 Human pot
43	502.5	24.0	294	6	ABG72802	ABG72802 Human 667
44	498.5	23.8	292	5	AAU99893	AAU99893 Rat potas
45	498.5	23.8	292	5	AAU99894	AAU99894 Mouse pot

## ALIGNMENTS

RESULT 1  
AAV34133  
ID AAV34133 standard; protein; 411 AA.  
XX  
AC AAV34133;  
XX  
DT 30-NOV-1999 (first entry)  
XX  
DE Human potassium channel K-Hnov59.  
XX  
KW Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;  
KW Cardiovascular disorder; CNS disorder; renal disorder.  
XX  
OS Homo sapiens.  
XX  
PN W09943696-A1.  
XX  
PR 02-SEP-1999.  
XX  
PF 22-FEB-1999; 99WO-US003826.  
XX  
PR 25-FEB-1998; 98US-0076687P.  
PR 07-AUG-1998; 98US-0095836P.  
PR 19-JAN-1999; 99US-0116448P.  
XX  
PA (AXYS-) AXYS PHARM INC.  
PI Miller AP, Curran ME, Hu P, Rutter M, Wang J;  
DR WPI, 1999-527591/44.  
DR N-PSDB; AA211915.  
PT New nucleic acid encoding mammalian K-Hnov potassium channel proteins,  
PT useful for the diagnosis and treatment of episodic ataxia with myokymia,  
PT cardiac arrhythmia, epilepsy and Bartter's syndrome.  
PI  
PS Claim 3; Page 104-105; 112pp; English.  
XX  
PS This sequence represents the human K-Hnov59 potassium channel. K-Hnov  
XX proteins have a high degree of homology to known potassium channels and  
XX may be alpha subunits, which form the functional channel, or accessory  
XX subunits that act to modulate the channel activity. K-Hnov59 is a 4  
XX transmembrane domain, 2 pore domain potassium channel. The gene is  
XX located on chromosome 19, determined via PCR chromosomal localisation  
XX using primers AA211939 and AA211940. K-Hnov cDNAs were isolated by  
XX extension of expressed sequence tags (ESTs) which were related but not  
XX identical to known human potassium channels. Potential polymorphisms  
XX detected as sequence variants between multiple independent clones.

CC Potassium channels have critical roles in various cell types and  
 CC biochemical pathways. Defective potassium channels are known to cause  
 CC four human diseases: episodic ataxia with myokymia; cardiac arrhythmia  
 CC (long QT syndrome); epilepsy; and Bartter's syndrome. As potassium  
 CC channels are critical components of virtually all cells, it is likely  
 CC that abnormal potassium channels are also implicated in certain renal,  
 CC cardiovascular and central nervous system (CNS) disorders. Nucleotides  
 CC encoding K-Hov proteins may be used for identifying homologous or  
 CC related proteins and the DNA sequences encoding them. They may be used to  
 CC produce compositions that modulate the expression and function of the  
 CC K-Hov protein and in studying the biochemical pathways associated with  
 CC it. They may also be used for the recombinant production of K-Hov  
 CC protein in fermentation cultures. Additionally, such nucleotides may be  
 CC used in gene therapy protocols for the treatment of diseases associated  
 CC with abnormal potassium channels

CC Sequence 411 AA;

Query Match 100.0%; Score 2098; DB 2; Length 411;

Best Local Similarity 100.0%; Pred. No. 1.4e-208; Mismatches 0; Gaps 0;

Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINMKKTVSTIFLVVLYLI 60  
 QY 61 GATVFKALEOPHEISQRTTIVIOKQTFISQHSQVNSTELDELIOQIVAINAGIIPLGNT 120  
 DB 61 GATVFKALEOPHEISQRTTIVIOKQTFISQHSQVNSTELDELIOQIVAINAGIIPLGNT 120  
 QY 121 SNOISHMDLSSFFPFGVITITIGFQNSIPRTEGKIFCIITVALLGIFLPGFLAGVGDQ 180  
 DB 121 SNOISHMDLSSFFPFGVITITIGFQNSIPRTEGKIFCIITVALLGIFLPGFLAGVGDQ 180  
 QY 181 LGTIFPGKIAKVEDTPIKKNVSQTKIRIISTIIIFLPGCVLPAIPAIIFKHIBGWSALD 240  
 DB 181 LGTIFPGKIAKVEDTPIKKNVSQTKIRIISTIIIFLPGCVLPAIPAIIFKHIBGWSALD 240  
 QY 241 AIFVAVITLTITIGFGDYVAGSDIEYLDYKPVWFWIIVGLAYPAAVLSMIGDMLRVIS 300  
 DB 241 AIFVAVITLTITIGFGDYVAGSDIEYLDYKPVWFWIIVGLAYPAAVLSMIGDMLRVIS 300  
 QY 301 KKTKEVGEFRAAAEWNTAVTAEPKETRRLSVEIYDKFORATSIKRLSALAGNHNQ 360  
 DB 301 KKTKEVGEFRAAAEWNTAVTAEPKETRRLSVEIYDKFORATSIKRLSALAGNHNQ 360  
 QY 361 ELTPCRRITLSVNHLTSESDVLPPLKTBESIYINGLTPHCAGEIIVNIENIK 411  
 DB 361 ELTPCRRITLSVNHLTSESDVLPPLKTBESIYINGLTPHCAGEIIVNIENIK 411

RESULT 2

AAV28496 standard; protein; 411 AA.

AC AAV28496;  
 DT 12-OCT-1999 (first entry)  
 DE h-TREK1 polypeptide.  
 DE h-TREK1, two pore potassium channel; inflammatory disease;  
 KM chromosome 1q32.  
 OS Homo sapiens.  
 PN WO9937762-A1.  
 PD 29-JUL-1999.  
 PF 02-DEC-1998; 98WO-EP007805.  
 PR 27-JAN-1998; 98EP-00300570.

FR 09-OCT-1998; 98GB-00022135.  
 XX (SMIK ) SMITHKLINE BEECHAM PLC.  
 PA Meadows HT, Chapman CG;  
 PI WPI; 1999-469126/39.  
 DR N-PSDB; AA200039.  
 XX New two pore potassium channel used for, e.g. treatment of cancer,  
 PT pulmonary, cardiovascular and inflammatory diseases.  
 PS Claim 3; Page 24; 44pp: English.

XX This sequence is the h-TREK1 polypeptide, encoded by the h-TREK1  
 CC polynucleotide AA200039. h-TREK1 is a two pore potassium channel, and the  
 CC gene maps to human chromosome 1q32, between the markers DIS237 and  
 CC W15105. The polynucleotide sequence of h-TREK1 can be used to diagnose a  
 CC disease or susceptibility to a disease related to expression or activity  
 CC of h-TREK1 polypeptides. The methods of diagnosis may be used in the  
 CC treatment of diseases including cancer, pulmonary, cardiovascular, and  
 CC inflammatory diseases, pain, psychiatric disorders including depression  
 CC and schizophrenia, neurodegenerative diseases including Alzheimer's,  
 CC stroke, and head trauma and neurological disorders including migraine

SO Sequence 411 AA;

Query Match 100.0%; Score 2098; DB 2; Length 411;

Best Local Similarity 100.0%; Pred. No. 1.4e-208; Mismatches 0; Gaps 0;

Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINMKKTVSTIFLVVLYLI 60  
 QY 61 GATVFKALEOPHEISQRTTIVIOKQTFISQHSQVNSTELDELIOQIVAINAGIIPLGNT 120  
 DB 61 GATVFKALEOPHEISQRTTIVIOKQTFISQHSQVNSTELDELIOQIVAINAGIIPLGNT 120  
 QY 121 SNOISHMDLSSFFPFGVITITIGFQNSIPRTEGKIFCIITVALLGIFLPGFLAGVGDQ 180  
 DB 121 SNOISHMDLSSFFPFGVITITIGFQNSIPRTEGKIFCIITVALLGIFLPGFLAGVGDQ 180  
 QY 181 LGTIFPGKIAKVEDTPIKKNVSQTKIRIISTIIIFLPGCVLPAIPAIIFKHIBGWSALD 240  
 DB 181 LGTIFPGKIAKVEDTPIKKNVSQTKIRIISTIIIFLPGCVLPAIPAIIFKHIBGWSALD 240  
 QY 241 AIFVAVITLTITIGFGDYVAGSDIEYLDYKPVWFWIIVGLAYPAAVLSMIGDMLRVIS 300  
 DB 241 AIFVAVITLTITIGFGDYVAGSDIEYLDYKPVWFWIIVGLAYPAAVLSMIGDMLRVIS 300  
 QY 301 KKTKEVGEFRAAAEWNTAVTAEPKETRRLSVEIYDKFORATSIKRLSALAGNHNQ 360  
 DB 301 KKTKEVGEFRAAAEWNTAVTAEPKETRRLSVEIYDKFORATSIKRLSALAGNHNQ 360  
 QY 361 ELTPCRRITLSVNHLTSESDVLPPLKTBESIYINGLTPHCAGEIIVNIENIK 411  
 DB 361 ELTPCRRITLSVNHLTSESDVLPPLKTBESIYINGLTPHCAGEIIVNIENIK 411

RESULT 3

AAAB50044 standard; protein; 411 AA.

AC AAB50044;  
 DT 19-MAR-2001 (first entry)  
 DE Human TREK.  
 DE Human, TREK; 2P domain potassium channel; reeling membrane potential;  
 KM neuronal excitability; neurotransmitter release modulation; epilepsy;  
 KM neurological disorder; sleep-related disorder; cognitive dysfunction;

KM attention deficit disorder; addiction; anxiety; phobia;  
KM Parkinson's chorea; Huntington's chorea; cerebral palsy; incontinence;  
KM erectile dysfunction; alopecia.  
XX  
XX Homo sapiens.  
XX  
XX WO200072863-A2.  
XX  
XX 07-DEC-2000.  
XX  
XX 01-JUN-2000; 2000WO-GB002107.  
XX  
XX 01-JUN-1999; 99GB-00012733.  
XX  
XX (SMIK ) SMITHKLINE BEECHAM PLC.  
XX  
XX Hervieu GJ, Meadows HJ, Randall AD;  
XX  
XX WPI; 2001-080422/09.  
XX  
XX N-PSDB; AAC90412.  
XX  
XX Use of human TREK1 polypeptide, polynucleotides encoding them and  
PT modulators of h-TREK1 polypeptides for treating epilepsy, sleep-related  
PT disorders, addiction and dyskinesias including Parkinson's and  
PT Huntington's chorea.  
XX  
XX  
XX Claim 7; Page 29; 35pp; English.  
XX  
XX The present sequence is human TREK1 (h-TREK1). h-TREK1 is a member of the  
CC 2P domain potassium channel family of proteins which play a part in the  
CC control of resting membrane potential. Modulation of these channels will  
CC therefore affect neuronal excitability, thereby leading to a modulation  
CC of neurotransmitter release and activity of neuronal networks. Such  
CC modulation therefore may be useful for the treatment of certain  
CC neurological conditions such as epilepsy, sleep-related disorders,  
CC cognitive dysfunction, attention deficit disorder, addiction,  
CC anxiety/phobia, Parkinson's and Huntington's chorea, cerebral palsy,  
CC incontinence, erectile dysfunction or alopecia  
XX  
XX Sequence 411 AA;  
XX  
XX Query Match 100.0%; Score 2098; DB 4; Length 411;  
XX Best Local Similarity 100.0%; Pred. No. 1.4e-208;  
XX Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINMKKKTSTIFLVVLYLI 60  
XX 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINMKKKTSTIFLVVLYLI 60  
XX  
XX  
XX 61 GATVFKALBOPHEISORTTIVIOKOTFISQHSVNSTELDELIOQIVAAINAGIIPLGNT 120  
XX  
XX 61 GATVFKALBOPHEISORTTIVIOKOTFISQHSVNSTELDELIOQIVAAINAGIIPLGNT 120  
XX  
XX 121 SNOISHMDLGSSEFFPAGTIVITTFGNIISPRETEGKIFCIYALLGIPFGFLAGVGDQ 180  
XX  
XX 121 SNOISHMDLGSSEFFPAGTIVITTFGNIISPRETEGKIFCIYALLGIPFGFLAGVGDQ 180  
XX  
XX 121 SNOISHMDLGSSEFFPAGTIVITTFGNIISPRETEGKIFCIYALLGIPFGFLAGVGDQ 180  
XX  
XX 121 SNOISHMDLGSSEFFPAGTIVITTFGNIISPRETEGKIFCIYALLGIPFGFLAGVGDQ 180  
XX  
XX 181 LGTIFGKGIKIAVEDTFIKMNSQTKIRIISTIFILFGCVLFVLPALPFIKHIIEGWSALD 240  
XX  
XX 181 LGTIFGKGIKIAVEDTFIKMNSQTKIRIISTIFILFGCVLFVLPALPFIKHIIEGWSALD 240  
XX  
XX 181 LGTIFGKGIKIAVEDTFIKMNSQTKIRIISTIFILFGCVLFVLPALPFIKHIIEGWSALD 240  
XX  
XX 241 AIFEVVITLTITIGFGDYVAGGSDIEYDFKPVVWFWILVGLAYFAAVLSMIGDMLRVIS 300  
XX  
XX 241 AIFEVVITLTITIGFGDYVAGGSDIEYDFKPVVWFWILVGLAYFAAVLSMIGDMLRVIS 300  
XX  
XX 241 AIFEVVITLTITIGFGDYVAGGSDIEYDFKPVVWFWILVGLAYFAAVLSMIGDMLRVIS 300  
XX  
XX 301 KKTKEVEGEFRRAAEWTANVTAEFEKTERRLSVEIYDKFQZATSIKRLSALAGNHNQ 360  
XX  
XX 301 KKTKEVEGEFRRAAEWTANVTAEFEKTERRLSVEIYDKFQZATSIKRLSALAGNHNQ 360  
XX  
XX 301 KKTKEVEGEFRRAAEWTANVTAEFEKTERRLSVEIYDKFQZATSIKRLSALAGNHNQ 360  
XX  
XX 361 ELTPCRRTLSEVNHLSERDYLPLLKTRESIYLANGLPFHQAGEIAVIEINIK 411  
XX  
XX 361 ELTPCRRTLSEVNHLSERDYLPLLKTRESIYLANGLPFHQAGEIAVIEINIK 411  
XX  
XX 361 ELTPCRRTLSEVNHLSERDYLPLLKTRESIYLANGLPFHQAGEIAVIEINIK 411

RESULT 4  
ID AAE10341  
XX AAE10341 standard; protein, 411 AA.  
XX  
XX AAE10341;  
XX  
XX 10-DEC-2001 (first entry)  
XX  
XX Human TREK-1 potassium channel protein.  
XX  
XX Human TREK-1 potassium channel protein; TREK-1; anaesthetic; analgesia;  
KM amnesia.  
XX  
XX Homo sapiens.  
XX  
XX WO200047738-A2.  
XX  
XX 17-AUG-2000.  
XX  
XX 11-FEB-2000; 2000WO-IB000226.  
XX  
XX 12-FEB-1999; 99US-0119727P.  
XX  
XX 11-FEB-2000; 2000US-00503089.  
XX  
XX (CNRS ) CNRS CENT NAT RECH SCI.  
XX  
XX Lazdunski M, Honore E, Lesage F, Romey G, Patel AJ;  
XX  
XX WPI; 2000-549146/50.  
XX  
XX N-PSDB; AAD17496.  
XX  
XX Novel nucleic acid encoding a TREK-1 potassium channel protein for  
PT transfecting cells to be used to identify compounds with anaesthetic  
PT properties.  
XX  
XX Claim 3; Page 28; 35pp; English.  
XX  
XX The invention relates to human and mouse TREK-1 potassium channel  
CC proteins and their corresponding DNA molecules. TREK-1 nucleic acid is  
CC useful for transfecting cells to induce expression of the TREK-1  
CC potassium channel protein. These cells are then used in assays to  
CC identify compounds which have anaesthetic properties, producing a safe,  
CC reversible state of unconsciousness with concurrent amnesia and analgesia  
CC in a mammal upon inhalation. The present sequence is human TREK-1  
CC potassium channel protein  
XX  
XX Sequence 411 AA;  
XX  
XX Query Match 99.9%; Score 2095; DB 3; Length 411;  
XX Best Local Similarity 99.8%; Pred. No. 2.9e-208;  
XX Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINMKKKTSTIFLVVLYLI 60  
XX 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINMKKKTSTIFLVVLYLI 60  
XX  
XX  
XX 61 GATVFKALBOPHEISORTTIVIOKOTFISQHSVNSTELDELIOQIVAAINAGIIPLGNT 120  
XX  
XX 61 GATVFKALBOPHEISORTTIVIOKOTFISQHSVNSTELDELIOQIVAAINAGIIPLGNT 120  
XX  
XX 121 SNOISHMDLGSSEFFPAGTIVITTFGNIISPRETEGKIFCIYALLGIPFGFLAGVGDQ 180  
XX  
XX 121 SNOISHMDLGSSEFFPAGTIVITTFGNIISPRETEGKIFCIYALLGIPFGFLAGVGDQ 180  
XX  
XX 121 SNOISHMDLGSSEFFPAGTIVITTFGNIISPRETEGKIFCIYALLGIPFGFLAGVGDQ 180  
XX  
XX 121 SNOISHMDLGSSEFFPAGTIVITTFGNIISPRETEGKIFCIYALLGIPFGFLAGVGDQ 180  
XX  
XX 181 LGTIFGKGIKIAVEDTFIKMNSQTKIRIISTIFILFGCVLFVLPALPFIKHIIEGWSALD 240  
XX  
XX 181 LGTIFGKGIKIAVEDTFIKMNSQTKIRIISTIFILFGCVLFVLPALPFIKHIIEGWSALD 240  
XX  
XX 181 LGTIFGKGIKIAVEDTFIKMNSQTKIRIISTIFILFGCVLFVLPALPFIKHIIEGWSALD 240  
XX  
XX 241 AIFEVVITLTITIGFGDYVAGGSDIEYDFKPVVWFWILVGLAYFAAVLSMIGDMLRVIS 300  
XX  
XX 241 AIFEVVITLTITIGFGDYVAGGSDIEYDFKPVVWFWILVGLAYFAAVLSMIGDMLRVIS 300  
XX  
XX 241 AIFEVVITLTITIGFGDYVAGGSDIEYDFKPVVWFWILVGLAYFAAVLSMIGDMLRVIS 300

QY 301 KKTKEVGEFRAHAAMWTAVTAEFKETRRLSVETIYDKFORATSIRKLSAELAGNHQ 360  
 DB 301 KKTKEVGEFRAHAAMWTAVTAEFKETRRLSVETIYDKFORATSIRKLSAELAGNHQ 360  
 QY 361 ELTPCRRITLSVNLTSERDVLPLLKTBSIYNGLTTPHCGEIAIENIK 411  
 DB 361 ELTPCRRITLSVNLTSERDVLPLLKTBSIYNGLTTPHCGEIAIENIK 411

RESULT 5  
 ID AAE16597 standard; protein; 411 AA.  
 XX AAE16597;

XX 18-APR-2002 (first entry)  
 DE Human TWIK-Related K<sup>+</sup> Channel-1 (TREK-1) protein.  
 XX Human; TWIK-Related K<sup>+</sup> Channel-1; TREK-1; anaesthetic; screening.  
 OS Homo sapiens.

XX Key Location/Qualifiers  
 FT Region 47..65  
 FT /note="M1 membrane spanning segment"  
 FT Domain 127..150  
 FT /note="P1 pore domain"  
 FT Region 158..178  
 FT /note="M2 membrane spanning segment"  
 FT Region 209..230  
 FT /note="M3 membrane spanning segment"  
 FT Domain 236..259  
 FT /note="P2 pore domain"  
 FT Region 274..293  
 FT /note="M4 membrane spanning segment"

XX WO200200715-A2.

XX 03-JAN-2002.

XX 27-JUN-2001; 2001WO-IB001436.

XX 27-JUN-2000; 2000US-0214559P.

XX 27-JUN-2001; 2001US-00892360.

XX (CNRS ) CNRS CENT NAT RECH SCI.

XX Lazdunski M, Lesage F, Romey G;

XX WPI; 2002-139903/18.

XX New mammalian K<sup>+</sup> channel protein with two pore domains, for screening  
 PT various compounds, particularly for identifying biologically active  
 PT compounds with anesthetic properties.

XX Disclosure; Fig 1A; 50pp; English.

XX The invention relates to a mammalian K<sup>+</sup> channel protein with two pore  
 CC domains, called TREK2 (TWIK-Related K<sup>+</sup> Channel). The protein produces  
 CC currents whose current-voltage relationship is slightly inwardly  
 CC rectifying in high symmetrical K<sup>+</sup> conditions. TREK2 is a member of the  
 CC fatty acid-activated and mechanosensitive K<sup>+</sup> channel family. TREK-2 gene  
 CC located on chromosome 14q31 is abundantly expressed in kidney, pancreas  
 CC and moderately in testis, brain, colon and small intestine. The mammalian  
 CC K<sup>+</sup> channel protein is useful in methods for screening various compounds.  
 CC In particular, the protein is useful in methods for identifying  
 CC biologically active compounds with anesthetic properties. The present  
 CC sequence is TREK-1 protein used in the invention

XX Sequence 411 AA;

Query Match 99.5%; Score 2087; DB 5; Length 411;

Best Local Similarity 99.5%; Pred. No. 2e-207; Indels 0; Gaps 0;  
 Matches 409; Conservative 1; Mismatches 1;

QY 1 MAAPDLIDPKSAQNSKPRLSFSTKPTVLASRVESDTTINWKKTVSTIFLVVLYLI 60  
 DB 1 MAAPDLIDPKSAQNSKPRLSFSTKPTVLASRVESDTTINWKKTVSTIFLVVLYLI 60  
 QY 61 GATVPKALBOPHESQRTTIVIOKOTFISQSCVNSTEDLLOIQAIAINAGIPLGNT 120  
 DB 61 GATVPKALBOPHESQRTTIVIOKOTFISQSCVNSTEDLLOIQAIAINAGIPLGNT 120  
 QY 121 SNOISHWDLSSFPFAGVTITIGFNTSPRTGKIFCIYALGIPFGFLAGVQD 180  
 DB 121 SNOISHWDLSSFPFAGVTITIGFNTSPRTGKIFCIYALGIPFGFLAGVQD 180  
 QY 121 SNOISHWDLSSFPFAGVTITIGFNTSPRTGKIFCIYALGIPFGFLAGVQD 180  
 DB 121 SNOISHWDLSSFPFAGVTITIGFNTSPRTGKIFCIYALGIPFGFLAGVQD 180  
 QY 181 LGTIFGKIAKVEDTIFKNNVSTKRIISTIFIFPGCVLPVALPAIIFKHIEGMSAD 240  
 DB 181 LGTIFGKIAKVEDTIFKNNVSTKRIISTIFIFPGCVLPVALPAIIFKHIEGMSAD 240  
 QY 241 AIYFVVTITLTIGFGYVAGGSDIEYLDPKPVPMFIIWGLAYFAAVLSMIGDLRVIS 300  
 DB 241 AIYFVVTITLTIGFGYVAGGSDIEYLDPKPVPMFIIWGLAYFAAVLSMIGDLRVIS 300  
 QY 301 KKTKEVGEFRAHAAMWTAVTAEFKETRRLSVETIYDKFORATSIRKLSAELAGNHQ 360  
 DB 301 KKTKEVGEFRAHAAMWTAVTAEFKETRRLSVETIYDKFORATSIRKLSAELAGNHQ 360  
 QY 361 ELTPCRRITLSVNLTSERDVLPLLKTBSIYNGLTTPHCGEIAIENIK 411  
 DB 361 ELTPCRRITLSVNLTSERDVLPLLKTBSIYNGLTTPHCGEIAIENIK 411

RESULT 6  
 ID AAU07618 standard; protein; 426 AA.  
 XX AAU07618;

XX 21-NOV-2001 (first entry)

XX Human potassium ion channel TPIC1 protein.

XX Transmembrane potassium ion channel protein; inward potassium flux;  
 KW pest control; membrane potential; pesticide; antihelminthic; nematode;  
 KW insect; TPIC1; human.

XX Homo sapiens.

XX WO200161006-A2.

XX 23-AUG-2001.

XX 14-FEB-2001; 2001WO-US004680.

XX 15-FEB-2000; 2000US-00503849.

XX (BADI ) BASF CORP.

XX Pausch ME;

XX WPI; 2001-536570/59.

XX N-PSDB; AAS12169.

XX New polypeptide, a mutant potassium ion channel protein for improving  
 PT inward potassium flux under acidic conditions.

XX Example 15; Page 45; 131pp; English.

XX The invention relates to a mutant potassium ion channel protein, having  
 CC four membrane spanning domains and two pore forming domains, comprising a  
 CC mutation at the second pore forming domain. The expression of the mutant  
 CC protein in a cell confers improved inward potassium flux and the ability  
 CC to grow in the presence of potassium. Mutant proteins and their

CC corresponding polynucleotide sequences can therefore be used to improve  
 CC inward potassium flux into cells under acidic conditions by modulating  
 CC the membrane potential using therapeutic agents. The sequences may be  
 CC used to develop agonists and antagonists of potassium channel proteins in  
 CC order to control pests such as nematodes and insects. This sequence  
 CC represents a human transmembrane potassium ion channel protein, TPKC1  
 XX  
 XX Sequence 426 AA;

Query Match 98.4%; Score 2065; DB 4; Length 426;  
 Best Local Similarity 98.8%; Pred. No. 4e-205;  
 Matches 406; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MAAPDLDPKSAQNSKPRLSFTKPTVLASRVESDTTINVMKKTIVSTIFLVVLYLI 60  
 DB 16 VAAPDLDPKSAQNSKPRLSFTKPTVLASRVESDTTINVMKKTIVSTIFLVVLYLI 75  
 QY 61 GATVFKALDQPHISQRTTIVIQKQTFISQSCVNSTELDELIQOIIVAANAGIIPLGNT 120  
 DB 76 GATVFKALDQPHISQRTTIVIQKQTFISQSCVNSTELDELIQOIIVAANAGIIPLGNT 135  
 QY 121 SNOISHMDLGSSFFPAGVITTTIGFNGISPRTEGKIFCIITVALGIPFGFLAGVDQ 180  
 DB 136 SNOISHMDLGSSFFPAGVITTTIGFNGISPRTEGKIFCIITVALGIPFGFLAGVDQ 195  
 QY 181 LGTIFGKGIKAVEDTFTKMNVSQTKRIISTITIFLFGCVLPAALPKHIEGMSALD 240  
 DB 196 LGTIFGKGIKAVEDTFTKMNVSQTKRIISTITIFLFGCVLPAALPKHIEGMSALD 255  
 QY 241 AIYFVVTITTTIGFDYVAGGSDIEYLDFFKPYVWFILVGLAFAVLSMTIGMLRVIS 300  
 DB 256 AIYFVVTITTTIGFDYVAGGSDIEYLDFFKPYVWFILVGLAFAVLSMTIGMLRVIS 315  
 QY 301 KKTKEVGEFPAHAAMWTANTVTAFFKETRRRLSVEIYDKFORATSIKRLSAELAGNHQ 360  
 DB 316 KKTKEVGEFPAHAAMWTANTVTAFFKETRRRLSVEIYDKFORATSIKRLSAELAGNHQ 375  
 QY 361 ELTPCRRLTSVNLTSERDVPPLKTESIYNGLTFFHCAGEEIAVENIK 411  
 DB 376 ELTPCRRLTSVNLTSERDVPPLKTESIYNGLTFFHCAGEEIAVENIK 426

## RESULT 7

AAU07622 standard; protein; 426 AA.

XX AC AAU07622;  
 XX DT 21-NOV-2001 (first entry)  
 XX DE Human potassium ion channel TPKC1 mutant protein #1.  
 XX KW Transmembrane potassium ion channel protein; inward potassium flux;  
 XX pest control; membrane potential; pesticide; antihelminthic; nematode;  
 XX insect; TPKC1; human; mutant; mutein.  
 XX OS Homo sapiens.  
 XX FT Key Location/Qualifiers  
 FT Misc-difference 256 /note= "wild-type Ala replaced by Thr"

XX WO200161006-A2.

XX 23-AUG-2001.

XX 14-FEB-2001; 2001WO-US004680.

XX 15-FEB-2000; 2000US-00503849.

XX (BADI ) BASF CORP.

XX PA Pausch WH;

XX PI

XX WP1; 2001-536570/59.  
 DR N-PSDB; AAS12181.

XX PT New polypeptide, a mutant potassium ion channel protein for improving  
 PT inward potassium flux under acidic conditions.

XX PS Claim 37; Page 113-115; 131pp; English.

XX The invention relates to a mutant potassium ion channel protein, having  
 CC four membrane spanning domains and two pore forming domains, comprising a  
 CC mutation at the second pore forming domain. The expression of the mutant  
 CC protein in a cell confers improved inward potassium flux and the ability  
 CC to grow in the presence of potassium. Mutant proteins and their  
 CC corresponding polynucleotide sequences can therefore be used to improve  
 CC inward potassium flux into cells under acidic conditions by modulating  
 CC the membrane potential using therapeutic agents. The sequences may be  
 CC used to develop agonists and antagonists of potassium channel proteins in  
 CC order to control pests such as nematodes and insects. This sequence  
 CC represents a human transmembrane potassium ion channel TPKC1 mutant  
 CC protein

XX SQ Sequence 426 AA;

Query Match 98.2%; Score 2061; DB 4; Length 426;  
 Best Local Similarity 98.5%; Pred. No. 1e-204;  
 Matches 405; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAAPDLDPKSAQNSKPRLSFTKPTVLASRVESDTTINVMKKTIVSTIFLVVLYLI 60  
 DB 16 VAAPDLDPKSAQNSKPRLSFTKPTVLASRVESDTTINVMKKTIVSTIFLVVLYLI 75  
 QY 61 GATVFKALDQPHISQRTTIVIQKQTFISQSCVNSTELDELIQOIIVAANAGIIPLGNT 120  
 DB 76 GATVFKALDQPHISQRTTIVIQKQTFISQSCVNSTELDELIQOIIVAANAGIIPLGNT 135  
 QY 121 SNOISHMDLGSSFFPAGVITTTIGFNGISPRTEGKIFCIITVALGIPFGFLAGVDQ 180  
 DB 136 SNOISHMDLGSSFFPAGVITTTIGFNGISPRTEGKIFCIITVALGIPFGFLAGVDQ 195  
 QY 181 LGTIFGKGIKAVEDTFTKMNVSQTKRIISTITIFLFGCVLPAALPKHIEGMSALD 240  
 DB 196 LGTIFGKGIKAVEDTFTKMNVSQTKRIISTITIFLFGCVLPAALPKHIEGMSALD 255  
 QY 241 AIYFVVTITTTIGFDYVAGGSDIEYLDFFKPYVWFILVGLAFAVLSMTIGMLRVIS 300  
 DB 256 TTYFVVTITTTIGFDYVAGGSDIEYLDFFKPYVWFILVGLAFAVLSMTIGMLRVIS 315  
 QY 301 KKTKEVGEFPAHAAMWTANTVTAFFKETRRRLSVEIYDKFORATSIKRLSAELAGNHQ 360  
 DB 316 KKTKEVGEFPAHAAMWTANTVTAFFKETRRRLSVEIYDKFORATSIKRLSAELAGNHQ 375  
 QY 361 ELTPCRRLTSVNLTSERDVPPLKTESIYNGLTFFHCAGEEIAVENIK 411  
 DB 376 ELTPCRRLTSVNLTSERDVPPLKTESIYNGLTFFHCAGEEIAVENIK 426

## RESULT 8

AAU07623 standard; protein; 426 AA.

XX AAU07623;

XX DT 21-NOV-2001 (first entry)

XX DE Human potassium ion channel TPKC1 mutant protein #2.

XX KW Transmembrane potassium ion channel protein; inward potassium flux;  
 KW pest control; membrane potential; pesticide; antihelminthic; nematode;  
 KW insect; TPKC1; human; mutant; mutein.

XX OS Homo sapiens.

```

FH Key Location/Qualifiers
FT Misc-difference 272 /note= "Wild-type Tyr replaced by His"
XX
XX
XX PN W0200161006-A2.
XX
XX PD 23-AUG-2001.
XX
XX PF 14-FEB-2001; 2001WO-US004680.
XX
XX PR 15-FEB-2000; 2000US-00503849.
XX
XX PA (BAD1 ) BASF CORP.
XX
XX PI Pausch MH;
XX
XX DR WPI; 2001-536570/59.
XX
XX DR N-PSDB; AAS12182.
XX
XX PT New polypeptide, a mutant potassium ion channel protein for improving
XX inward potassium flux under acidic conditions.
XX
XX PS Claim 37; Page 115-117; 131pp; English.
XX
XX CC The invention relates to a mutant potassium ion channel protein, having
XX four membrane spanning domains and two pore forming domains, comprising a
XX mutation at the second pore forming domain. The expression of the mutant
XX protein in a cell confers improved inward potassium flux and the ability
XX to grow in the presence of potassium. Mutant proteins and their
XX corresponding polynucleotide sequences can therefore be used to improve
XX inward potassium flux into cells under acidic conditions by modulating
XX the membrane potential using therapeutic agents. The sequences may be
XX used to develop agonists and antagonists of potassium channel proteins in
XX order to control pests such as nematodes and insects. This sequence
XX represents a human transmembrane potassium ion channel TPKC1 mutant
XX protein
XX
XX SQ Sequence 426 AA;

Query Match 98.2%; Score 2060; DB 4; Length 426;
Best Local Similarity 98.5%; Pred. No. 1.3e-204;
Matches 405; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MAAPDLIDPKSAONSKPRLSFSTKPTVLASRVESDTTINWKKMTVSTIFLVVLYLI 60
DB :
DB 16 VAAPDLIDPKSAONSKPRLSFSTKPTVLASRVESDTTINWKKMTVSTIFLVVLYLI 75
QY 61 GATVFALDQPHISQRTTIVIOKQTFISQHSQVNSTEDELIOQIVAAINAGIIPLGNT 120
DB :
DB 76 GATVFALDQPHISQRTTIVIOKQTFISQHSQVNSTEDELIOQIVAAINAGIIPLGNT 135
QY 121 SNOISHMDGSSFFFGAGTIVITIGFNGISPRTEGGKIFCIYALGIPFGFLAGVGDQ 180
DB :
DB 136 SNOISHMDGSSFFFGAGTIVITIGFNGISPRTEGGKIFCIYALGIPFGFLAGVGDQ 195
QY 181 LGTIFGKGIAXVEDFTIKMNVSQTKIRIISTIFILFGCVLFAVPAIIFKHIBGWSALD 240
DB :
DB 196 LGTIFGKGIAXVEDFTIKMNVSQTKIRIISTIFILFGCVLFAVPAIIFKHIBGWSALD 255
QY 241 AAYFVVTITTTIGFGDYVAGSDIEYLDPKFVWFMLVGLAYFAAVALSMIGDLRYIS 300
DB :
DB 256 AAYFVVTITTTIGFGDYVAGSDIEYLDPKFVWFMLVGLAYFAAVALSMIGDLRYIS 315
QY 301 KKTKEVGEFRAHAAEWMTANVTAEFKETRRRLSVEIYDKFORATSIKKLSAELAGNHNQ 360
DB :
DB 316 KKTKEVGEFRAHAAEWMTANVTAEFKETRRRLSVEIYDKFORATSIKKLSAELAGNHNQ 375
QY 361 ELTPGRTLSVNHLSERDVPPELLKTESIYNGLTPEHCAGEIAVENIK 411
DB :
DB 376 ELTPGRTLSVNHLSERDVPPELLKTESIYNGLTPEHCAGEIAVENIK 426

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RESULT 9

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AAU07625
ID AAU07625 standard; protein; 426 AA.
XX
XX AC AAU07625;
XX
XX AC 21-NOV-2001 (first entry)
XX
XX DE Human potassium ion channel TPKC1 mutant protein #4.
XX
XX KW Transmembrane potassium ion channel protein; inward potassium flux;
XX pest control; membrane potential; pesticide; antihelminthic; nematode;
XX insect; TPKC1; human; mutant; mutein.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 270 /note= "Wild-type Gly replaced by Arg"
XX
XX PN W0200161006-A2.
XX
XX PD 23-AUG-2001.
XX
XX PF 14-FEB-2001; 2001WO-US004680.
XX
XX PR 15-FEB-2000; 2000US-00503849.
XX
XX PA (BAD1 ) BASF CORP.
XX
XX PI Pausch MH;
XX
XX DR WPI; 2001-536570/59.
XX
XX DR N-PSDB; AAS12184.
XX
XX PT New polypeptide, a mutant potassium ion channel protein for improving
XX inward potassium flux under acidic conditions.
XX
XX PS Claim 37; Page 119-120; 131pp; English.
XX
XX CC The invention relates to a mutant potassium ion channel protein, having
XX four membrane spanning domains and two pore forming domains, comprising a
XX mutation at the second pore forming domain. The expression of the mutant
XX protein in a cell confers improved inward potassium flux and the ability
XX to grow in the presence of potassium. Mutant proteins and their
XX corresponding polynucleotide sequences can therefore be used to improve
XX inward potassium flux into cells under acidic conditions by modulating
XX the membrane potential using therapeutic agents. The sequences may be
XX used to develop agonists and antagonists of potassium channel proteins in
XX order to control pests such as nematodes and insects. This sequence
XX represents a human transmembrane potassium ion channel TPKC1 mutant
XX protein
XX
XX SQ Sequence 426 AA;

Query Match 98.0%; Score 2057; DB 4; Length 426;
Best Local Similarity 98.5%; Pred. No. 2.7e-204;
Matches 405; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAAPDLIDPKSAONSKPRLSFSTKPTVLASRVESDTTINWKKMTVSTIFLVVLYLI 60
DB :
DB 16 VAAPDLIDPKSAONSKPRLSFSTKPTVLASRVESDTTINWKKMTVSTIFLVVLYLI 75
QY 61 GATVFALDQPHISQRTTIVIOKQTFISQHSQVNSTEDELIOQIVAAINAGIIPLGNT 120
DB :
DB 76 GATVFALDQPHISQRTTIVIOKQTFISQHSQVNSTEDELIOQIVAAINAGIIPLGNT 135
QY 121 SNOISHMDGSSFFFGAGTIVITIGFNGISPRTEGGKIFCIYALGIPFGFLAGVGDQ 180
DB :
DB 136 SNOISHMDGSSFFFGAGTIVITIGFNGISPRTEGGKIFCIYALGIPFGFLAGVGDQ 195
QY 181 LGTIFGKGIAXVEDFTIKMNVSQTKIRIISTIFILFGCVLFAVPAIIFKHIBGWSALD 240
DB :
DB 196 LGTIFGKGIAXVEDFTIKMNVSQTKIRIISTIFILFGCVLFAVPAIIFKHIBGWSALD 255

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OY 241 AIFVITLTITIGFDYVAGSDIEYDFKPVWFWMLVGLAYFAVLISMIGDLRVIS 300
DB 256 AIFVITLTITIGFRYVAGSDIEYDFKPVWFWMLVGLAYFAVLISMIGDLRVIS 315
OY 301 KTKKEVEGFRRAHAEMWTANVTAEFKETRRRLSVEIYDKFORATSIKRLSALAGNHQ 360
DB 316 KTKKEVEGFRRAHAEMWTANVTAEFKETRRRLSVEIYDKFORATSIKRLSALAGNHQ 375
OY 361 ELTPCRRTLSVNHLSERDVLPLPKTESIYVGLTPHCGEELAVENIK 411
DB 376 ELTPCRRTLSVNHLSERDVLPLPKTESIYVGLTPHCGEELAVENIK 426

RESULT 10
AAU07624
ID AAU07624 standard; protein; 426 AA.
XX
AC AAU07624;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human potassium ion channel TPKC1 mutant protein #3.
XX
KM Transmembrane potassium ion channel protein; inward potassium flux;
KW pest control; membrane potential; pesticide; antihelminthic; nematode;
OS insect; TPKC1; human; mutant; mutcin.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 272 /note= "Wild-type Tyr replaced by His"
FT Misc-difference 274 /note= "Wild-type Ala replace by Val"
FT FT
XX
XX MO200161006-A2.
XX
PD 23-AUG-2001.
XX
PF 14-FEB-2001; 2001WO-US004680.
XX
PR 15-FEB-2000; 2000US-00503849.
XX
PA (BADI ) BASP CORP.
PI Pausch MH;
XX
DR WPI; 2001-536570/59.
DR N-PSDB; AAS12183.
XX
PT New polypeptide, a mutant potassium ion channel protein for improving
PT inward potassium flux under acidic conditions.
XX
PS Claim 37; Page 117-119; 13pp; English.
XX
XX The invention relates to a mutant potassium ion channel protein, having
XX four membrane spanning domains and two pore forming domains, comprising a
XX mutation at the second pore forming domain. The expression of the mutant
XX protein in a cell confers improved inward potassium flux and the ability
XX to grow in the presence of potassium. Mutant proteins and their
XX corresponding polynucleotide sequences can therefore be used to improve
XX inward potassium flux into cells under acidic conditions by modulating
XX the membrane potential using therapeutic agents. The sequences may be
XX used to develop agonists and antagonists of potassium channel proteins in
XX order to control pests such as nematodes and insects. This sequence
XX represents a human transmembrane potassium ion channel TPKC1 mutant
XX protein
XX
SQ Sequence 426 AA;
XX
Query Match 98.0%; Score 2056; DB 4; Length 426;
Best Local Similarity 98.3%; Pred. No. 3.4e-204;

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Matches 404; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
OY 1 MAAPDLIDPKSAQNSKPRLSFSTKPTVLASRYESDPTINMKKTVSTFLVVLII 60
DB 16 VAAPDLIDPKSAQNSKPRLSFSTKPTVLASRYESDPTINMKKTVSTFLVVLII 75
OY 61 GAIVFKALEQPHHSQRTTIVIOKQTFISQHSQVNSTELDELIOQIVAAINAGIIPLGNT 120
DB 76 GAIVFKALEQPHHSQRTTIVIOKQTFISQHSQVNSTELDELIOQIVAAINAGIIPLGNT 135
OY 121 SNOISHMDLSSPFPAQTIVITIGFNIISPRTEGKIFCIIVALLGIFGFLLAGVDQ 180
DB 136 SNOISHMDLSSPFPAQTIVITIGFNIISPRTEGKIFCIIVALLGIFGFLLAGVDQ 195
OY 181 LGTIFGKGIKVEDTFIKMNVISQTKIRIISTIIIFILGCVLPVALPAIIFKHIEGMSALD 240
DB 196 LGTIFGKGIKVEDTFIKMNVISQTKIRIISTIIIFILGCVLPVALPAIIFKHIEGMSALD 255
OY 241 AIFVITLTITIGFDYVAGSDIEYDFKPVWFWMLVGLAYFAVLISMIGDLRVIS 300
DB 256 AIFVITLTITIGFDYVAGSDIEYDFKPVWFWMLVGLAYFAVLISMIGDLRVIS 315
OY 301 KTKKEVEGFRRAHAEMWTANVTAEFKETRRRLSVEIYDKFORATSIKRLSALAGNHQ 360
DB 316 KTKKEVEGFRRAHAEMWTANVTAEFKETRRRLSVEIYDKFORATSIKRLSALAGNHQ 375
OY 361 ELTPCRRTLSVNHLSERDVLPLPKTESIYVGLTPHCGEELAVENIK 411
DB 376 ELTPCRRTLSVNHLSERDVLPLPKTESIYVGLTPHCGEELAVENIK 426

RESULT 11
AAE10342
ID AAE10342 standard; protein; 411 AA.
XX
AC AAE10342;
XX
DT 10-DEC-2001 (first entry)
XX
DE Murine TREK-1 potassium channel protein.
XX
KM Murine; potassium channel protein; TREK-1; anaesthetic; analgesia;
KW amnesia.
XX
OS Mus musculus.
XX
PN WO200047738-A2.
XX
PD 17-AUG-2000.
XX
PF 11-FEB-2000; 2000WO-IB000226.
XX
PR 12-FEB-1999; 99US-0119727P.
PR 11-FEB-2000; 2000US-00503089.
XX
PA (CNRS ) CNRS CENT NAT RECH SCI.
PI Lazdunski M, Honore F, Lesage F, Romey G, Patel AJ;
XX
DR WPI; 2000-549146/50.
DR N-PSDB; AAD17497.
XX
PT Novel nucleic acid encoding a TREK-1 potassium channel protein for
PT transfecting cells to be used to identify compounds with anesthetic
PT properties.
XX
PS Claim 9; Page 32-33; 39pp; English.
XX
XX The invention relates to human and mouse TREK-1 potassium channel
XX proteins and their corresponding DNA molecules. TREK-1 nucleic acid is
XX useful for transfecting cells to induce expression of the TREK-1
XX potassium channel protein. These cells are then used in assays to
XX identify compounds which have anaesthetic properties, producing a safe,

```

CC reversible state of unconsciousness with concurrent amnesia and analgesia  
CC in a mammal upon inhalation. The present sequence is murine TREK-1  
CC potassium channel protein  
XX

SO Sequence 411 AA;

Query Match 97.4%; Score 2044; DB 3; Length 411;  
Best Local Similarity 96.4%; Pred. No. 5.7e-203;  
Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESPTTNMWMKTVSTIFLVVLYLII 60  
DB 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESPTTNMWMKTVSTIFLVVLYLII 60  
QY 61 GATVFKALBOPHISQRTTIVIQKTFISQSCVNSTELDELIQIVAAINAGIPLNGT 120  
DB 61 GAATVFKALBOPHISQRTTIVIQKTFISQSCVNSTELDELIQIVAAINAGIPLNGS 120  
QY 121 SNQISHMDLGSFFFGVITTTGFGNISPRTGGKIFCIYVALLGIFLFGFLAGVGDQ 180  
DB 121 SNQISHMDLGSFFFGVITTTGFGNISPRTGGKIFCIYVALLGIFLFGFLAGVGDQ 180  
QY 181 LGTIFGKGIAXVEDTIFKNNVSQTKIRIISTIFILFGCVLFVALPAVIFKHEGMSALD 240  
DB 181 LGTIFGKGIAXVEDTIFKNNVSQTKIRIISTIFILFGCVLFVALPAVIFKHEGMSALD 240  
QY 241 AIFVAVITLTITGFGDYVAGSDIEYLDYKPVWFWIIVGLAFAVLSMTGDLRVIS 300  
DB 241 AIFVAVITLTITGFGDYVAGSDIEYLDYKPVWFWIIVGLAFAVLSMTGDLRVIS 300  
QY 301 KKTKEVGEFRAHAEMTANVTAEFKETRRRLSVEIYDKFORATSIKRKLASBLAGNNO 360  
DB 301 KKTKEVGEFRAHAEMTANVTAEFKETRRRLSVEIYDKFORATSIVKRLASBLAGNNO 360  
QY 361 ELTPCRRITLSVNLHLSERDVLPPLKTESIYINGLTPHCAGEIIVENIK 411  
DB 361 ELTPCRRITLSVNLHLSERDVLPPLKTESIYINGLTPHCAGEIIVENIK 411

RESULT 12

ID AAY28497 standard; protein; 411 AA.

XX AAY28497;  
AC AAY28497;  
XX  
DT 12-OCT-1999 (first entry)  
XX  
DE Mouse h-TREK1 polypeptide.  
XX  
KW h-TREK1, two pore potassium channel; inflammatory disease;  
KW chromosome 1q32.  
XX  
OS Mus. musculus.  
XX  
PN WO9937762-A1.  
PD 29-JUL-1999.  
XX  
PF 02-DEC-1998; 98WO-EP007805.  
XX  
PR 27-JAN-1998; 98EP-00300570.  
PR 09-OCT-1998; 98GB-00022135.  
XX

PA (SMK) SMITHKLINE BEECHAM PLC.

PI Meadows HJ, Chapman CG;

XX WPI; 1999-469126/39.

DR N-PSDB; AAC0040.

PT New two pore potassium channel used for, e.g. treatment of cancer,  
PT pulmonary, cardiovascular and inflammatory diseases.  
XX

PS Claim 3; Page 26; 44pp; English.

XX This sequence is the mouse h-TREK1 polypeptide, encoded by the h-TREK1  
CC polynucleotide AA200040. h-TREK1 is a two pore potassium channel. The  
CC polynucleotide sequence of h-TREK1 can be used to diagnose a disease or  
CC susceptibility to a disease related to expression or activity of h-TREK-1  
CC polypeptides. The methods of diagnosis may be used in the treatment of  
CC diseases including cancer, pulmonary, cardiovascular, and inflammatory  
CC diseases, pain, psychiatric disorders including depression and  
CC schizophrenia, neurodegenerative diseases including Alzheimer's, stroke,  
CC and head trauma and neurological disorders including migraine  
XX

SO Sequence 411 AA;

Query Match 97.1%; Score 2038; DB 2; Length 411;  
Best Local Similarity 96.1%; Pred. No. 2.4e-202;  
Matches 395; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESPTTNMWMKTVSTIFLVVLYLII 60  
DB 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESPTTNMWMKTVSTIFLVVLYLII 60  
QY 61 GATVFKALBOPHISQRTTIVIQKTFISQSCVNSTELDELIQIVAAINAGIPLNGT 120  
DB 61 GAATVFKALBOPHISQRTTIVIQKTFISQSCVNSTELDELIQIVAAINAGIPLNGS 120  
QY 121 SNQISHMDLGSFFFGVITTTGFGNISPRTGGKIFCIYVALLGIFLFGFLAGVGDQ 180  
DB 121 SNQISHMDLGSFFFGVITTTGFGNISPRTGGKIFCIYVALLGIFLFGFLAGVGDQ 180  
QY 181 LGTIFGKGIAXVEDTIFKNNVSQTKIRIISTIFILFGCVLFVALPAVIFKHEGMSALD 240  
DB 181 LGTIFGKGIAXVEDTIFKNNVSQTKIRIISTIFILFGCVLFVALPAVIFKHEGMSALD 240  
QY 241 AIFVAVITLTITGFGDYVAGSDIEYLDYKPVWFWIIVGLAFAVLSMTGDLRVIS 300  
DB 241 AIFVAVITLTITGFGDYVAGSDIEYLDYKPVWFWIIVGLAFAVLSMTGDLRVIS 300  
QY 301 KKTKEVGEFRAHAEMTANVTAEFKETRRRLSVEIYDKFORATSIKRKLASBLAGNNO 360  
DB 301 KKTKEVGEFRAHAEMTANVTAEFKETRRRLSVEIYDKFORATSIVKRLASBLAGNNO 360  
QY 361 ELTPCRRITLSVNLHLSERDVLPPLKTESIYINGLTPHCAGEIIVENIK 411  
DB 361 ELTPCRRITLSVNLHLSERDVLPPLKTESIYINGLTPHCAGEIIVENIK 411

RESULT 13

ID AAY30648 standard; protein; 370 AA.

XX AAY30648;  
AC AAY30648;  
XX  
DT 18-NOV-1999 (first entry)  
XX  
DE A mechanically sensitive potassium channel protein TREK-1.  
XX

XX Mechanically sensitive potassium channel protein; TREK-1;  
KW polyunsaturated fatty acid; arachidonic acid; riluzole; heart disease;  
KW nervous system disease; epilepsy; cardiovascular disease; arrhythmia;  
KW neurodegeneration; ischemia; anoxia; hormone secretion abnormality;  
KW muscular disease.  
XX

OS Mus sp.

XX WO9945108-A2.

XX 10-SEP-1999.

XX 23-FEB-1999; 99WO-FR000404.

XX 05-MAR-1998; 98FR-00002725.  
XX



PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX  
 PI Honore E, Fink M, Lazdunski M, Lesage F, Duprat F;  
 XX  
 DR WPI; 1999-551038/46.  
 DR N-PSDB; AAZ10607.  
 XX  
 PT New mechanically sensitive potassium channel, used to screen for specific  
 PT modulators, potential therapeutic agents for heart and nervous system  
 PT disorders.  
 XX  
 PS Claim 3; Page 23-25; 40pp; French.  
 XX  
 CC The present sequence represents a mechanically sensitive potassium  
 CC channel protein designated TREK-1. The protein is activated by  
 CC polyunsaturated fatty acids, particularly arachidonic acid, and by  
 CC riluzole. The protein is used to screen for specific modulators which are  
 CC useful for treating or preventing diseases of the heart and nervous  
 CC systems in humans and animals, e.g. epilepsy, cardiovascular disease  
 CC (arrhythmia), neurodegeneration (particularly where associated with  
 CC ischemia or anoxia), abnormalities of hormone secretion and muscular  
 CC disease. The protein itself may be used to treat these diseases.  
 CC Antibodies specific for the protein are used to detect it in tissues,  
 CC also as therapeutic inhibitors or activators  
 CC  
 XX  
 SQ Sequence 370 AA;  
 XX  
 QY Query Match 87.4%; Score 1833; DB 2; Length 370;  
 Best Local Similarity 96.7%; Pred. No. 3, 9e-181;  
 Matches 355; Conservative 8; Mismatches 4; Indels 0; Gaps 0;  
 XX  
 QY 1 MAAPDLIDPKSAQAQNSKRLSFTSKPTVLASRVESDTTNVMMKTVSTIFLVVLYLII 60  
 1 MAAPDLIDPKSAQAQNSKRLSFTSKPTVLASRVESDTTNVMMKTVSTIFLVVLYLII 60  
 DB 1 MAAPDLIDPKSAQAQNSKRLSFTSKPTVLASRVESDTTNVMMKTVSTIFLVVLYLII 60  
 QY 61 GAIVFKALBEPHISQRTTIVIKQRTFISCHSCVNSTEDLIIQOVAIINNGIIFLQNT 120  
 61 GAIVFKALBEPHISQRTTIVIKQRTFISCHSCVNSTEDLIIQOVAIINNGIIFLQNT 120  
 DB 61 GAIVFKALBEPHISQRTTIVIKQRTFISCHSCVNSTEDLIIQOVAIINNGIIFLQNT 120  
 QY 121 SNOISHMDLGSSEFFAGTVITTTIGFQNSIPRTGKIFCIIVALLGIPFGLLAGVQDQ 180  
 121 SNOISHMDLGSSEFFAGTVITTTIGFQNSIPRTGKIFCIIVALLGIPFGLLAGVQDQ 180  
 DB 121 SNOISHMDLGSSEFFAGTVITTTIGFQNSIPRTGKIFCIIVALLGIPFGLLAGVQDQ 180  
 QY 181 LGTIFGKIGAKVDDPTFKMWSQTKRIITSTIFIFGCVLPALPAIIPKHEGMSAID 240  
 181 LGTIFGKIGAKVDDPTFKMWSQTKRIITSTIFIFGCVLPALPAIIPKHEGMSAID 240  
 DB 181 LGTIFGKIGAKVDDPTFKMWSQTKRIITSTIFIFGCVLPALPAIIPKHEGMSAID 240  
 QY 241 AIFVFWITLTITIGFGDVAGSDIEYLDPFYKPVWFMIVGLAYFAAVISMIGDWLRVIS 300  
 241 AIFVFWITLTITIGFGDVAGSDIEYLDPFYKPVWFMIVGLAYFAAVISMIGDWLRVIS 300  
 DB 241 AIFVFWITLTITIGFGDVAGSDIEYLDPFYKPVWFMIVGLAYFAAVISMIGDWLRVIS 300  
 QY 301 KKTKEVEGFRRAHAAEWTANVTAEFKETRRRLSVEIYDKFORATSIKTKLSAELAGNNHQ 360  
 301 KKTKEVEGFRRAHAAEWTANVTAEFKETRRRLSVEIYDKFORATSIKTKLSAELAGNNHQ 360  
 DB 301 KKTKEVEGFRRAHAAEWTANVTAEFKETRRRLSVEIYDKFORATSIKTKLSAELAGNNHQ 360  
 QY 361 ELTPCRRRT 368  
 361 ELTPCRRRT 368  
 DB 361 ELTPCRRRT 368  
 XX  
 RESULT 14  
 ABR41487  
 ID ABR41487 standard; protein; 337 AA.  
 XX  
 AC ABR41487;  
 DT 02-JUN-2003 (first entry)  
 XX  
 DE Human DITHP membrane transport protein.  
 XX  
 KW Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;  
 KW cancer; cell proliferative disorder; autoimmune disorder;  
 KW inflammatory disorder; infection; hormonal disorder; metabolic disorder;

KW neurological disorder; gastrointestinal disorder; transport disorder;  
 KW connective tissue disorder; drug screening; proteome analysis;  
 KW gene therapy; antisense therapy; genotyping; transgenic animal; knock in;  
 KW disease model; toxicological testing; transcript imaging;  
 KW membrane transport protein.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200297031-A2.  
 XX  
 PD 05-DEC-2002.  
 XX  
 PF 27-MAR-2002; 2002WO-US010056.  
 XX  
 PR 28-MAR-2001; 2001US-0279619P.  
 XX  
 PR 29-MAR-2001; 2001US-0280067P.  
 XX  
 PR 29-MAR-2001; 2001US-0280068P.  
 XX  
 PR 16-MAY-2001; 2001US-0291280P.  
 XX  
 PR 17-MAY-2001; 2001US-0291829P.  
 XX  
 PR 17-MAY-2001; 2001US-0291849P.  
 XX  
 PR 19-JUN-2001; 2001US-0299428P.  
 XX  
 PR 20-JUN-2001; 2001US-0299776P.  
 XX  
 PR 20-JUN-2001; 2001US-0300001P.  
 XX  
 PA (INCYTE GENOMICS INC.  
 XX  
 PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;  
 PI Dufour GE, Hillman JL, Yu JT, Tuason O, Yap PP, Amthey SR;  
 PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleeefeld Y, Gerstin EH;  
 PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;  
 PI Flores V, Marwana R, Lo A, Lan RY, Urashka ME;  
 DR WPI; 2003-129518/12.  
 DR N-PSDB; ACC46425.  
 XX  
 PT Novel human diagnostic and therapeutic polypeptide useful for identifying  
 PT test compound which specifically binds to a polypeptide encoded by human  
 PT diagnostic and therapeutic polynucleotide, and to induce antibodies.  
 XX  
 PS Claim 27; SEQ ID NO 1022; 591pp; English.  
 XX  
 CC The invention relates to novel human diagnostic and therapeutic  
 CC polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded  
 CC proteins (DITHP, ABR41136-ABR41812). The invention also relates to  
 CC polynucleotide sequences at least 90% identical to the dithp cDNA  
 CC sequences of the invention; recombinant vectors, host cells and  
 CC transgenic organisms comprising a dithp nucleic acid sequence; the  
 CC recombinant production of DITHP proteins; antibodies specific for DITHP  
 CC proteins; microarrays comprising dithp nucleic acid sequences; methods of  
 CC detecting dithp nucleotide and protein sequences; methods of screening  
 CC for compounds which specifically bind a DITHP protein; and methods of  
 CC assessing the toxicity of test compounds using a dithp hybridisation  
 CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the  
 CC diagnosis of a wide variety of conditions including cancer and other cell  
 CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,  
 CC viral, fungal or parasitic infections; hormonal disorders; metabolic  
 CC disorders; neurological disorders; gastrointestinal disorders; transport  
 CC disorders; and connective tissue disorders. They may also be used to  
 CC screen for modulators of protein activity or gene expression. DITHP  
 CC proteins can additionally be used in analysis of the proteome of a tissue  
 CC or cell type and to induce antibodies. The dithp nucleic acids are  
 CC additionally useful in somatic or germline gene therapy of the disorders  
 CC mentioned above, as a source of antisense sequences, as a source of  
 CC probes and primers, in genotyping and identification of individuals, in  
 CC the generation of transgenic animal models of human disease or knock in  
 CC humanised animals, in toxicological testing, and in transcript imaging.  
 CC The present sequence represents a DITHP protein which has membrane  
 CC transport protein activity. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pcr\_sequences  
 XX  
 SQ Sequence 337 AA;

Query Match 78.2%; Score 1641.5; DB 6; Length 337;  
 Best Local Similarity 97.0%; Pred. No. 2.6e-161;  
 Matches 342; Conservative 2; Mismatches 7; Indels 1; Gaps 1;

QY 80 IVIQKOTFTSQHSCVNSTEDELIIQIVAINAGIIPLENTSNOISHWMDLSSPFFAGTV 139  
 DB 7 LVIQKHSHYPTPLC-HSTBELDELIIQIVAINAGIIPLENTSNOISHWMDLSSPFFAGTV 65  
 QY 140 ITTIGFNTSPRTGSKIFCIYIYALIGPLFGFLAGVGDQGITFGKGIANVEDTFTKM 199  
 DB 66 ITTIGFNTSPRTGSKIFCIYIYALIGPLFGFLAGVGDQGITFGKGIANVEDTFTKM 125  
 QY 200 NVSOTIRITSTIIFLFGCVLFPALPFIKHEBMSALDIYVVIITLTIGFDYVA 259  
 DB 126 NVSOTIRITSTIIFLFGCVLFPALPFIKHEBMSALDIYVVIITLTIGFDYVA 185  
 QY 260 GGSIDIEYLPYKPVWFILVGLAFAVLISMGWLRVTSKKEBVEGFPAHAETWA 319  
 DB 186 GGSIDIEYLPYKPVWFILVGLAFAVLISMGWLRVTSKKEBVEGFPAHAETWA 245  
 QY 320 NTAERKERTRRRLSVIYDXFORATSIKRLSABELAGNNHDELTCRRLSVNHLTSRD 379  
 DB 246 NTAERKERTRRRLSVIYDXFORATSIKRLSABELAGNNHDELTCRRLSVNHLTSRD 305  
 QY 380 VLPPILKTESIYINGLTPRCAGEBIAVENIX 411  
 DB 306 VLPPILKTESIYINGLTPRCAGEBIAVENIX 337

## RESULT 15

AA047930  
 ID AAB47930 standard; protein; 538 AA.

XX AC AAB47930;  
 XX 10-JUN-2002 (first entry)  
 DT Human TREK2.  
 XX Human; K<sup>+</sup> channel; potassium; TREK2; pore domain; general anaesthetic;  
 KM neurotransmitter receptor.  
 XX Homo sapiens.  
 OS  
 FH Key Location/Qualifiers  
 FT Domain 72..90  
 FT /note="Membrane spanning domain 1"  
 FT 152..175  
 FT /note="Pore domain 1"  
 FT 183..203  
 FT /note="Membrane spanning domain 2"  
 FT 234..255  
 FT /note="Membrane spanning domain 3"  
 FT 261..284  
 FT /note="Pore domain 2"  
 FT 300..319  
 FT /note="Membrane spanning domain 4"

PN WO200200715-A2.

PD 03-JAN-2002.

PF 27-JUN-2001; 2001WO-1B001436.

PR 27-JUN-2000; 2000US-0214559P.

PR 27-JUN-2001; 2001US-00892360.

XX (CNRS) CNRS CENT NAT RECH SCI.

PI Lazdunski M, Lesage F, Romey G;

XX WPI, 2002-139903/18.

DR N-PSDB: AA172558.

XX New mammalian K<sup>+</sup> channel protein with two pore domains, for screening  
 PT various compounds, particularly for identifying biologically active  
 PT compounds with anaesthetic properties.

PS Claim 3; Page 44-46; 50pp; English.

CC This sequence shows a protein, which constitutes a human K<sup>+</sup> channel,  
 CC TREK2, which has two pore domains that produces currents whose current-  
 CC voltage relationship is slightly inwardly rectifying in high symmetrical  
 CC K<sup>+</sup> conditions. TREK2 is activated by general anaesthetics at clinical  
 CC concentrations. It is modulated by different types of neurotransmitter  
 CC receptors. The TREK2 gene produces a cDNA of 2730 bp which contains an  
 CC open reading frame of 1617 nucleotides. The TREK2 protein has the same  
 CC overall structure as previously described K<sup>+</sup> channels. It has four  
 CC membrane spanning domains (M1-M4), two pore domains (P1-P2) and an  
 CC extended loop between M1 and P1. TREK2 shares 63% identity and 78%  
 CC homology to TREK1. The chromosomal location of the TREK2 gene is 14q31.  
 CC TREK2 is useful in methods for screening various compounds. In  
 CC particular, the protein is useful in methods for identifying biologically  
 CC active compounds with anaesthetic properties

XX Sequence 538 AA;

Query Match 59.2%; Score 1242.5; DB 5; Length 538;  
 Best Local Similarity 63.5%; Pred. No. 1.3e-119;  
 Matches 244; Conservative 57; Mismatches 66; Indels 17; Gaps 5;

QY 2 AAPDLDPKSA-----AQNKRPLSFSTKPTVLAASVESDT--TINWKKTKVSTI 50  
 DB 17 AAPVCPKSKATNGQPPAPAPPTPRLSISRAVVA-RWEGTSQGLQVWKKTVVAI 75  
 QY 51 FLVVLVLIIGATVFAKLEQPHISORTIIVIQKTFISQHCVNSTEDELIIQIVAAI 110  
 DB 76 FVVVVVLYLVGAVFPALBQPFSSQKNTIALEKAFLELDHCVSQELETILIQALDAD 135  
 QY 111 NAGIIPLGNTSNOISHWMDLSSPFFAGTVITTTGFGNISPRTBGGKIFCIYIYALIGPLF 170  
 DB 136 NAGVSPGNSNNSSHWMDLSSPFFAGTVITTTGFGNISPRTBGGKIFCIYIYALIGPLF 195  
 QY 171 GFLLAGVGDQGITFGKGIANVEDTFTKMNVSOTKIRISTIIIFLFGCVLFPALPFI 230  
 DB 196 GFLLAGVGDQGITFGKGIANVEDTFTKMNVSOTKIRISTIIIFLFGCVLFPALPFI 255  
 QY 231 KHIEGSAIDAIYFVVIITLTIGFDYVAGG-SDIEYLPYKPVWFILVGLAFAVLA 289  
 DB 256 KYIEGWTALIESIYFVVIITLTIGFDYVAGGAGNAGINRYREMYKPLVFWILVGLAFAVLA 315  
 QY 290 SMIGDWLRVTSKKEBVEGFPAHAETWANTATAEKERTRRRLSVIYDXFORATSI--- 346  
 DB 316 SMIGDWLRVTSKKEBVEGFPAHAETWANTATAEKERTRRRLSVIYDXFORATSI--- 375  
 QY 347 -KRLSABELAGNNHDELTCRRL 369  
 DB 376 ERRRLGDDQRAHSLDMLSPKREV 399

Search completed: July 15, 2004, 17:59:23  
 Job time : 56 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 15, 2004, 17:58:13 ; Search time 16 Seconds  
(without alignments)  
2470.920 Million cell updates/sec

Title: US-09-980-350-2

Perfect score: 2098  
Sequence: 1 MAAPLDLPDKSAQNSKPERL.....LNGLPHCAGBEIAVENIK 411

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	379.5	18.1	336	2 S65566	inward rectifier p
2	347.5	16.6	330	2 JC7703	TASK-5 protein - h
3	345	16.4	329	2 T43509	probable potassium
4	331.5	15.8	336	2 T32347	outward rectifier
5	319	15.2	1001	2 T13807	potassium channel
6	288	13.7	383	2 T23182	hypothetical prote
7	284.5	13.6	334	2 T19860	hypothetical prote
8	284.5	13.6	364	2 T43361	probable potassium
9	283.5	13.5	461	2 T43394	potassium channel
10	279	13.3	393	2 T25392	hypothetical prote
11	273	13.0	392	2 T45032	hypothetical prote
12	273	13.0	1910	2 H88124	protein T12C9.3 f
13	269	12.8	325	2 T15584	hypothetical prote
14	265.5	12.7	522	2 T24265	hypothetical prote
15	262	12.5	452	2 T21118	hypothetical prote
16	249.5	11.9	427	2 T27681	hypothetical prote
17	247	11.8	444	2 T26229	hypothetical prote
18	245.5	11.7	1539	2 T30037	hypothetical prote
19	244.5	11.7	513	2 T28933	hypothetical prote
20	240	11.4	524	2 T23907	hypothetical prote
21	236	11.2	643	2 T26616	hypothetical prote
22	232	11.1	528	2 T21834	hypothetical prote
23	230	11.0	443	2 T21598	hypothetical prote
24	230	11.0	550	2 T22557	hypothetical prote
25	228.5	10.9	484	2 T43529	probable potassium
26	228.5	10.9	519	2 T16629	hypothetical prote
27	224	10.7	1136	2 T26953	hypothetical prote
28	220.5	10.5	551	2 T16426	hypothetical prote
29	220.5	10.5	555	2 T43357	potassium channel

30	218	10.4	307	2 H89074	protein twk-24 [im
31	218	10.4	485	2 T24201	hypothetical prote
32	217.5	10.4	335	2 S44635	f22b7.7 protein -
33	217.5	10.4	544	2 T43364	potassium channel
34	217.5	10.4	576	2 T43363	potassium channel
35	217.5	10.4	691	2 S46585	outward-rectifier
36	217	10.3	475	2 T27725	hypothetical prote
37	215.5	10.3	586	2 T21683	hypothetical prote
38	211	10.1	660	2 T21551	hypothetical prote
39	206.5	9.8	523	2 T23373	hypothetical prote
40	205.5	9.8	381	2 T43393	potassium channel
41	205.5	9.8	769	2 T27550	hypothetical prote
42	205	9.8	700	2 T27364	hypothetical prote
43	202.5	9.7	539	2 T23700	hypothetical prote
44	196	9.3	681	2 T19429	hypothetical prote
45	195	9.3	504	2 T22269	hypothetical prote

## ALIGNMENTS

RESULT 1  
S65566  
inward rectifier potassium channel TWIK-1 - human  
C.Species: Homo sapiens (man)  
C.Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 05-Nov-1999  
C.Accession: S65566  
Release, F.; Guillemare, E.; Fink, M.; Duprat, F.; Lazdunski, M.; Romey, G.; Barhanin, EMO J. 15, 1004-1011, 1996  
A>Title: TWIK-1, a ubiquitous human weakly inward rectifying K(+) channel with a novel s  
A.Reference number: S65566; MUID:96183184; PMID:8605869  
A.Accession: S65566  
A.Status: preliminary  
A.Molecule type: mRNA  
A.Residues: 1-336 <LES>  
A.Cross-references: EMBL:U33632; NID:G1066490; PID:AB01688.1; PID:G1086491

Query Match 18.1%; Score 379.5; DB 2; Length 336;  
Best Local Similarity 32.5%; Pred. No. 2.4e-23;  
Matches 90; Conservative 62; Mismatches 108; Indels 17; Gaps 9;

QY 51 FLVV--VYLTIGTVFALKEOPHEISORTIVQKOFESCHSGVNSTEDLIQOVA 108  
DB 25 FLVGLYLLVLFAGVAFSVLPEDILRQRLKRFLEHRLCSQQLGRVLE 84  
QY 109 AINAGIIPLGNTSNQISHMDLGSFFPAGVITTTIGFNTSPRTGGKIFCIYALGIP 168  
DB 85 ASNVGVSVLSNAGSN-WNWDFTSLAFASVTLSTGYCHTVPLSDGKAFCIIVSGLIP 143  
QY 169 LFGFLAAGVQQLGTFKKGIAKYEDRTIKNNVSGTKRIISTII--FILFGCVLFAVLP 226  
DB 144 FTLLFLFAVGRITVHVR--RPVLYFPIRNGFSKQVAIVHVALGLGVTSVCFPI--P 199  
QY 227 AIFFGHIE-GWSALDAIFYGVITTTIGFGDYVAG-GSDIEYLPFYKPVVFMILVGLAY 284  
DB 200 AAFVSVLDDNNFLESFFCFISLSTIGLGYVGEGRNQKFRRELYKNGICIVYLLGLIA 259  
QY 285 FAAVISMTGMDLRVTSK----KTKEEVGEPRAHAE 316  
DB 260 MLVVLTEPCE-LHELKFRKMFYVKDDEQVHIE 295

RESULT 2  
JC7703  
TASK-5 protein - human  
C.Species: Homo sapiens (man)  
C.Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 09-Nov-2001  
C.Accession: JC7703  
R.Kim, D.; Gnatenko, C.  
Biochem. Biophys. Res. Commun. 284, 923-930, 2001  
A>Title: TASK-5, a new member of the tandem-pore K+ channel family.  
A.Reference number: JC7703; MUID:21303050; PMID:11409881  
A.Accession: JC7703



RESULT 6  
T23182  
hypothetical protein K01D12.4 - *Caenorhabditis elegans*  
C|Species: *Caenorhabditis elegans*  
C|Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C|Accession: T23182  
R|Dobson, R.  
submitted to the EMBL Data Library, June 1996  
A|Reference number: Z19703  
A|Accession: T23182  
A|Status: preliminary; translated from GB/EMBL/DBJ  
A|Molecule type: DNA  
A|Residues: 1..383 <MBL>  
A|Cross-references: EMBL:Z75543; PIDN:CAA93871.1; GPSDB:GN00023; CESP:K01D12.4  
A|Experimental source: clone K01D12  
C|Genetics:  
A|Gene: CESP:K01D12.4  
A|Map position: 5  
A|Intons: 28/3; 76/3; 184/2; 217/2; 270/2; 295/2

[illegible]

Query Match	13.6%	Score 284.5;	DB 2;	Length 364;
Best Local Similarity	27.4%	Pred. No. 1.5e-15;		

Matches 86; Conservative 63; Mismatches 112; Indels 53; Gaps 11;

QY 50 IFIVVLYLIGATVFKALQEPHEISQRTIV---IQKQTFISQSCVNSTELDELIOOI 106  
 Db 14 LILSTFYLIFGAMVFDKLE-----SEKOTWDEIERITDRKHK-YNFSERDHLFPA 67  
 QY 107 VAAINAGIIPLGNTSNOISH-WDLGSSFFPAGVITTTIGFNGISPRTEGGKIFCIITALL 165  
 Db 68 IA-----IKSIPQAGQWQFAGAFYATVITTVGYSABPTNAGKIFCIITALL 119  
 QY 166 GILPFGFLAGVDQDGTIFGKIAIYVEDTFK-----WNSQTKIRIIS-TTIFILFG 218  
 Db 120 GVEMGIMFQGISBERVTFAYSLHKFRDLSHQGFTCLQEVYPTHTLWVSLTIGFMV-- 177  
 QY 219 CVLFLVLPALIFKHIGMSALDAIFVVTTLTTIGFGDYV--AGSGDIEYLDFFKPVWF 276  
 Db 178 ----YSGTVMFTTIKMSIFDYYTCMTTFSTIGGDLVPLQVNALDQGLYFATIM 233  
 QY 277 WILVGLAYFAAVISMIGDMLRVISKTKEEVGFRAHAAMWTANYAEKTRRLSVEI 336  
 Db 234 FILIGLAVFSACVNL-----VLGFMAENADEVTA-----AQREPPSAIV 273  
 QY 337 YDKFORATSIKRL 350  
 Db 274 LERFTNRLVDSOI 287

## RESULT 9

T43394  
 potassium channel chain n2p18 homolog - Caenorhabditis elegans  
 C/Species: Caenorhabditis elegans  
 C/Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jan-2000  
 C/Accession: T43394  
 R/Kunkel, M.T.; Salikoff, L.  
 submitted to the EMBL Data Library, August 1998  
 A/Description: Potassium channels in C. elegans.  
 A/Reference number: Z22479  
 A/Accession: T43394  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-461 <XUN>  
 A/Cross-references: EMBL:AF083650; PIDN:AC32861.1

Query Match 13.5%; Score 283.5; DB 2; Length 461;  
 Best Local Similarity 23.5%; Pred. No. 2,4e-15;

Matches 102; Conservative 69; Mismatches 134; Indels 129; Gaps 14;

QY 46 TVSTIF-----LVVLYLIGATVFKALQEPHEISQRTIVIQKQTFISQSCVN 95  
 Db 10 TILTFQKTFKGLPLIIVATLLGAWIFWMEGSE-----REMIEGQK--- 56  
 QY 96 STELDLILQOIYAIN-----AGIIPLGNTSNOIS 125  
 Db 57 --ERDELIRRYKINOLOIKQORLMTAEEYNTAKVLTTFQRTIGIVPA--DMXD 112  
 QY 126 HMDLGSSFFPAGVITTTIGFNGISPRTEGGKIFCIITALL;PLFGFLAGVDQDGTIF 185  
 Db 113 HMFPLGSIYCMVITTVTIGVNIIVPOTGKGRATILYAFIGLPLVLSLY-----CLGSLF 168  
 QY 186 GKCIAYVEDTFIKVANSQTKIRIIS----- 210  
 Db 169 AGGCKMLMFRFLK-----STRVVSQDLSNKSIEADNIEGTATITPSAEKTENNDD 222  
 QY 211 ----TIFILFGCVLPALIPALIFKHIGMSALDAIFVVTTLTTIGFGDYVAGSDIEYL 267  
 Db 223 LSPFIFGLLITVIVITFCVNLFTPLIEBDFGTSLYFTLISITTTIGFGDILP--SDYFM 280  
 QY 268 DFYKPVVFWIIVGLAYFAVLSMIGDMLRVISKTKEEVGFRAHA-----AEWTAN 320  
 Db 281 ----PIVGVLLIIGLSLVSTVMTLLIOQIEALASGKNIDQEVARALNEAREDEVDEN 336  
 QY 321 VVAEFETRRRLSVELYDKFORATSIKRLSLAELAGNNQELTP-----CRRTISVNL 374

Db 337 VDPEDEPNKKSPDAY--ISRMWMSKGLYLLPDSQKELAKQSEKMGKRSIKIQ-- 392

QY 375 TSEPDVLPPLIKTE 388

Db 393 -TDNDLLETLLIREE 405

## RESULT 10

T25392  
 hypothetical protein T29A8.1 - Caenorhabditis elegans  
 C/Species: Caenorhabditis elegans  
 C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C/Accession: T25392  
 R.Lloyd, C.  
 submitted to the EMBL Data Library, March 1997

A/Reference number: Z20027

A/Accession: T25392

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA  
 A/Residues: 1-393 <WLL>  
 A/Cross-references: EMBL:Z92813; PIDN:CAB07286.1; GSPDB:GN00021; CESP:T29A8.1  
 A/Experimental source: clone T29A8

C/Genetics:  
 A/Map position: 3  
 A/Introns: 73/1; 112/3; 209/3; 287/2; 310/3; 364/2

Query Match 13.3%; Score 279; DB 2; Length 393;  
 Best Local Similarity 27.0%; Pred. No. 4,7e-15;  
 Matches 81; Conservative 54; Mismatches 107; Indels 58; Gaps 9;

QY 44 WKTVSTIFL-----VVVLYLIGATVFKALQEPHEISQRTIV---IQKQTFIS--- 89  
 Db 4 WKTVARILLHVLIVLVVYVGFAGFLFYOLEQEPHEVFRANIBRFNIHKQMEHL 63

QY 90 --QHSQSNSELDLILQOIYAINAGIPLGNT-----SNQISHMDLGSSFF 135  
 Db 64 EMRESGIGVHVEDLAKVYDNTTRILFAFDFHCAGKLRGSGEDDNTMTALTF 123

QY 136 AGVITTTIGFNGISPRTEGGKIFCIITALL;PLFGFLAGVD-----QLGTIFGK 188  
 Db 124 TTTLLTIGVGNLPTVGRKLCILYALFGVPLILITVADIGKFLSENIYQLTYWRKL 183

QY 189 IAYVEDTFIKVANSQTK-----IRISTIFILFGCVL--VVALPAILFKHI 233  
 Db 184 REKCSKQ--KYSVISKDDKNKEGDLNLDLENYISIPILIVAILLSYITFGAVALSNM 241

QY 234 EGMSALDAIFVVTTLTTIGFGDYVAGSDIEYLDFFKPVVFWIIVGLAYFAVLSMIG 293  
 Db 242 EGMDFSGFPRFSPTMTTVGFDIVPLKREYILDL-----CYITIGSITTMCTIDY 295

## RESULT 11

T45032  
 hypothetical protein Y39B8.f [imported] - Caenorhabditis elegans  
 C/Species: Caenorhabditis elegans  
 C/Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jul-2000

C/Accession: T45032  
 R/Willson, R.; Ainscough, R.; Anderson, K.; Baynes, C.; Berke, M.; Bonfield, J.; Burton, R.; O'Callaghan, M.; Parsons, J.; Percy, C.; Rifken, L.; Roopra, A.; Saunders, D.

Nature 368, 32-38, 1994  
 A/Authors: Showkeen, R.; Sims, M.; Smaidow, N.; Smith, A.; Smith, M.; Sonhammer, E.; S

lock, L.; Wilkinson-Sproat, J.; Wohlman, P.  
 A/Title: 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.

A/Reference number: S43531; M01D:94150718; PMID:7906398

A/Accession: T45032

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA  
 A/Residues: 1-392 <WLL>  
 A/Cross-references: EMBL:AL139896; NID:96434440; PIDN:CAB60911.1; PID:96434446

A/Experimental source: clone Y39B8  
 C/Genetics:

A:Map position: 3  
A:Intons: 47/2; 82/2; 106/3; 151/1; 220/1; 260/3; 370/3  
A:Note: Y39365.f

Query Match 13.0%; Score 273; DB 2; Length 392;  
Best Local Similarity 25.5%; Pred. No. 1.4e-14;  
Matches 83; Conservative 66; Mismatches 100; Indels 76; Gaps 13;

QY 7 LDRKSAQNS-----KPLRSFSTKPYLAS---RVESDTINVMKMKVSTIFLVVLY 57  
DB 64 LERHSKQSSLYPEKKAIAKESYSQDKTPKHFPPSKISLKLKAKRY----- 117  
QY 58 LIIGATVFKALEOPHEISQRTTIVIQKTFISQHS-----CVNSTELDELIOQI-V 107  
DB 118 -----FSRIEYPLE-----KIREAYLDYQNMWRDLIQLDIDSEIDKLPLNIRE 163  
QY 108 AAINAGIIPGNTSNQISHDSSFFPACTVTTTGPNISPRITGKIFCIYALGI 167  
DB 164 AALNGIMDMENLTD--PNMTFGQAFEFAGTLISTVGYGRVSPREYKGLFTILYCVIGI 221  
QY 168 PLFGFLAGV-----GDQGTIFGKGIKAVKEDPFIKMVSQTKIRLISIT 212  
DB 222 PLTLALISAVAMRSHKRLGLNORLGHF-----TNHIOQLIHVG 265  
QY 213 IFLLFGCVLFV-ALPAIIFPHIE-GMSALDAIFYVITLTITGFGDYVAGS-DIEYIDF 269  
DB 266 V-VFASILLFVFAIPAMVFSSIEFDWSYLDAPYCFVSLTTIGLDFEPGDPPNQFRL 324  
QY 270 YKPVVFWMLVGLAYFAAVLSMIGD 294  
DB 325 YKIGATVYLMGGLCCMMFLATLYD 349

RESULT 12  
H88124  
protein T12C9.3 [imported] - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 10-May-2001 #sequence\_revision 10-May-2001 #ext\_change 10-May-2001  
C/Accession: H88124  
R:anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology  
A:Reference number: A75000; MIMD:99069613; PMID:9851916  
A:Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_ele  
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
A:Accession: H88124  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1910 <STO>  
A:Cross-references: GB:chr\_II; PIDN:AC71141.1; PID:gl086770; GSPDB:GN00020; CESP:T12C9.3  
A:Note: proline-rich  
C:Genetics:  
A:Gene: T12C9.3  
A:Map position: 2

Query Match 13.0%; Score 273; DB 2; Length 1910;  
Best Local Similarity 23.3%; Pred. No. 9.8e-14;  
Matches 104; Conservative 74; Mismatches 122; Indels 146; Gaps 18;

QY 18 PRLS--FSTKPYLAS-RVESDTI---NVMKTVSTIFLVV---LYLIGATVFA 67  
DB 162 PQSSRRRSIFPGLLESARPDDETTTLQNRKXAKALPLHIVVVCIVATIGAWIFVT 221  
QY 68 LREQPHE-----ISQRTTIVIQKTFISQHSQVNSTEYD-----ELI-----Q 104  
DB 222 LESNENRRLKETGKRTIAEKRSNLIYK--INNEKEVKWEDIEKELMLYSEKLKYAFKE 278  
QY 105 QIVAINAGIIFL-----GNTSNQISH-----WDLGSSFFPAG 137  
DB 279 QYKRVSVRTIGFGRSSYEADETGSDSRKRRHGNKRGDSEKMMWTISSALFFFA 338  
QY 138 TVITTFGMSISPTBEGKIFCIYALGIPLFGFLAGVDGLG--TTF-----GKGLA 190

DB 339 TTMATIGNIVPVPILGRACVAFALFGADIALITIGDLKFLSECTIMLYKMRKGS 398  
QY 191 KVEDTFIKM-----NVSQTKILISITIFILFGCV 220  
DB 399 RLDSAWKFRGLEDSISDDLESASKNODSSILDMKDDEIKSEVPVLMVFITI-----L 452  
QY 221 LFVALPAIIFHIGESALDAIFYVITLTITGFGDYVAGSDIEYLDYKPVVFWMLV 280  
DB 453 LYIARGGILFSLIDMSYMDAFYFSFISLTITIGGDIYPENHD-----YAINLIYLG 506  
QY 281 GLAYFAVLSMIG-----DWLRVISKTK-----EYGEFFRAH 313  
DB 507 GLSVTTCIDLAGQYIQKIHFGFRKPGTDLLQYLKKRMLERBLAMGQGEETLRKYH 566  
QY 314 AAEWTANTAEFKSTRRLSVEIYDK 339  
DB 567 AVE-----KFERQEQLOQKMEB 585

RESULT 13  
T15584  
hypothetical protein C24A3.6 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #ext\_change 20-Sep-1999  
C/Accession: T15584  
R:Favella, T.  
submitted to: The EMBL Data Library, November 1995  
A:Description: The sequence of C. elegans cosmid C24A3.  
A:Reference number: Z18373  
A:Accession: T15584  
A>Status: preliminary; translated from GB/EMBL/DBU  
A:Molecule type: DNA  
A:Residues: 1-325 <FAV>  
A:Cross-references: EMBL:U0424; NID:gl065542; PID:gl065543; PIDN:AAA81455.1; CESP:C24A3  
C:Genetics:  
A:Gene: CESP:C24A3.6  
A:Intons: 21/1; 63/3; 131/1; 193/3; 206/3

Query Match 12.8%; Score 269; DB 2; Length 325;  
Best Local Similarity 25.1%; Pred. No. 2.4e-14;  
Matches 86; Conservative 53; Mismatches 88; Indels 116; Gaps 11;

QY 46 TVSTTF-----LVVLYLIGATVFALEQPHHISQRTTIVIQKTFISQHSQVN 95  
DB 10 TILTFQKTEKGLPLRLTILVAYTLIGAWIFMWIGENE-----REMLIEQOK-- 56  
QY 96 STELDELIOQIVAAIN-----AGIIPLGNTSNQIS 125  
DB 57 --ERREILRRFVYKINQIQIKQRRLMTAEERYNRKAKVLTTFQETLGIYVA--DMOKDI 112  
QY 126 HMDLSSSFFPACTVTTTGPNISPRITGKIFCIYALGIPLFGFLAGVQGLTIF 185  
DB 113 HMTPLGSIFFCMYVYTTIGYGNIVPGTGWGRFATILVAFIDPLVLSTV---CLGSLF 168  
QY 186 GKGIKVEDTFIKMVSQTKIRIIS----- 210  
DB 169 AKGCMMLRFLK-----STRVYSKLSNKSISDAADNIBEGTALTIPSAKTEENDD 222  
QY 211 --TIFILFGCVLFVALPAIIFHIGESALDAIFYVITLTITGFGDYVAGSDIEYL 267  
DB 223 LSPFISGLLITIVWIRCAVLFPLEWMDGTSLYFTLLISFTTIGGDIPL--SDYDFM 280  
QY 268 DFYKRVVFWMLVGLAYFAVLSMIGDWLRIS-----KTKKE 305  
DB 281 ---PIGVTLILIGLSVSTVMTLIIQOQIEALASVRRRRKKK 319

RESULT 14  
T24265  
hypothetical protein T01B4.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #ext\_change 18-Feb-2000  
C/Accession: T24265

R:Wilkinson, J.  
submitted to the EMBL Data Library, March 1996  
A/Reference number: Z19866  
A/Accession: T24265  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-522 <WIL>  
A/Cross-references: EMBL:Z70036; PIDN:CAA93875.1; GSPDB:GN00028; CESP:T01B4.1  
A/Experimental source: clone T01B4  
C/Genetics:  
A/Map position: X  
A/Introns: 95/3; 142/1; 224/3; 290/1; 458/1

Query Match 12.7%; Score 265.5; DB 2; Length 522;  
Best Local Similarity 23.4%; Pred. No. 8.4e-14;  
Matches 99; Conservative 63; Mismatches 132; Indels 129; Gaps 15;

QY 50 FLVVVLYLIIIGATVFKALEPHE-----ISQRTTIVIQKQTFISQSCVNSTE 98  
DB 41 LIIILIGVACLGGMVQALEVDQQLLEAEKRVRLSESSLLAVNLLEHLKQMCQSQNE 100  
QY 99 LDELIIQIYVAIINAGIIPLGNTS-NOISHMDLSSFFPAGTYITTTIGGNISPRTEGKI 157  
DB 101 -----RCLELITKTFIORSDEBERGEMWDFWNSVFSATLFTTIGYGNLACKTNLGR 155  
QY 158 FCIIYVALLGIPFGFLLAGVD-----OLGTFPGKG 188  
DB 156 ATIIYGMIGIPMLFLKXFGELCVMAKKIQENVOQCLKQGRKKQKASSLASITSKE 215  
QY 189 IAKV-----EDTF--IKMNSQTKRIRITSTIIFILPGCVLFVALPAIIFKAIIEGMS 237  
DB 216 MLEVFPEVEDDEKEDTTFQLRWG-----LVIVLFPVLCSPFVSPFWENWD 260  
QY 238 ALDAIFEVVITLTITGFGDYVAGGSDIEYDFYKPVWFWIL--VGLAVFAVLSMIGD- 294  
DB 261 FLTAFFYFFVSLSTIGFIVP-----DHPRTACALFVYFGLALFANVYAILDER 312  
QY 295 -----W-LRVISKTKKEVEGEFRAHAEMTANVT----- 322  
DB 313 VENQYVMALELIDQKQOEKLDQMYDEDEKADKNDMPKSKKEPYRGRILLQDLRSPD 372  
QY 323 AEFKETRRLS-----VEIYDQFORATSIKRLSAEL-----AGNHNQELTPCRRLTS 370  
DB 373 LKISGGRSSSDASSVITASDEDTNHFVGRAILLEAFAPDERASNHGTQLNSC--TVS 430  
QY 371 VNH 373  
DB 431 NEH 433

RESULT 15  
T21118  
hypotheical protein F19D8.1 - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 16-Feb-2000  
C/Accession: T21118  
R/Swinburne, J.; Ainscough, R.  
submitted to the EMBL Data Library, August 1996  
A/Reference number: Z19377  
A/Accession: T21118  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-452 <WIL>  
A/Cross-references: EMBL:Z78541; PIDN:CA801740.1; GSPDB:GN00028; CESP:F19D8.1  
A/Experimental source: clone F19D8  
C/Genetics:  
A/Map position: X  
A/Introns: 31/1; 82/2; 101/3; 157/1; 197/1; 230/3; 267/2; 325/3; 356/1; 404/3

Query Match 12.5%; Score 262; DB 2; Length 452;  
Best Local Similarity 28.5%; Pred. No. 1.4e-13;

Matches 81; Conservative 50; Mismatches 121; Indels 32; Gaps 7;  
QY 42 MKKWTSTI-----FLVVVLYLIIIGATVFKALE-----QPHISQRTTIVIQKQTFIS 89  
DB 36 MKRRNVLRILGHALAYCFVVCYFAGAWFFHQLEGENETELDKQREYAMLLKQVIAR 95  
QY 90 QHSCVNSTEDDELIIQIYVAIINAGIIPLGNTS-----TSNOISHMDLSSFFPAGTYITT 142  
DB 96 LATTENVAEINEHLRNFELRNISNLHISLDNYLIFNEPTQIVPRKWTFFPSVLSFTILTT 155  
QY 143 IFGNISPRTEGKIFCIYVALLGIPFGFLLAGVDQQLTIFGKIARVEDTFIKMNS 202  
DB 156 IGYGNVTPHTQCKVFEMITGAFGIPFLITTIADLGRFSKTAIMALVQKVSRELKQSD 215  
QY 203 QTKIRIISTI---IFILPGCVLFVALPAIIFKAIIEGM-----SALDAIFEVVITLTITGFG 255  
DB 216 EHLREIAEVSPLYDVLVAGLFFVFTALGSAVTPLEMQUTYFDSVITSYMSLTITIGG 275  
QY 256 DYVAGGSDIEYDFYKPVWFWILVGLAVFAVLSMIGDLRVT 299  
DB 276 DIVP-----RRMDFLLPTL-IYTTIGMLTTLALVEQLADVFRIV 313

Search completed: July 15, 2004, 18:01:04  
Job time: 17 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 15, 2004, 17:55:57 ; Search time 14 Seconds

(without alignments)  
1528.631 Million cell updates/sec

Title: US-09-980-350-2

Perfect score: 2098  
Sequence: 1 MAPDLDPKSAQNSKPRLL.....LNGLPFHGAGEIAVIENTIK 411

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2065	98.4	426	1	C1W2_HUMAN
2	2044	97.4	411	1	C1W2_MOUSE
3	1248.5	59.5	538	1	C1W2_RAT
4	1242.5	59.2	538	1	C1W2_HUMAN
5	803	38.3	333	1	C1W4_HUMAN
6	776.5	37.0	338	1	C1W4_MOUSE
7	502.5	24.0	309	1	C1W5_HUMAN
8	430	20.5	489	1	C1W5_HUMAN
9	393	18.7	332	1	C1W6_HUMAN
10	379.5	18.1	336	1	C1W1_HUMAN
11	370.5	17.7	336	1	C1W1_MOUSE
12	363	17.3	394	1	C1W3_HUMAN
13	357.5	17.0	365	1	C1W3_MOUSE
14	348	16.6	333	1	C1W6_HUMAN
15	347.5	16.6	330	1	C1W6_HUMAN
16	347.5	16.6	374	1	C1W3_HUMAN
17	343	16.3	409	1	C1W3_MOUSE
18	343	16.3	411	1	C1W3_RAT
19	328.5	15.7	237	1	C1W9_RAT
20	324.5	15.5	318	1	C1W6_RAT
21	319	15.2	1001	1	ORX1_DROME
22	307.5	14.7	430	1	C1W2_HUMAN
23	304	14.5	430	1	C1W2_RAT
24	296.5	14.1	307	1	C1W8_MOUSE
25	291.5	13.9	307	1	C1W1_HUMAN
26	282.5	13.5	408	1	C1W2_HUMAN
27	280	13.3	405	1	C1W2_RAT
28	278	13.3	405	1	C1W2_MOUSE
29	232	11.1	320	1	TKM7_CAEEL
30	217.5	10.4	691	1	TKM1_YEAST
31	159.5	7.6	443	1	KCO2_ARATH
32	147.5	7.0	408	1	KCO5_ARATH
33	143	6.8	246	1	KCO4_ARATH

## ALIGNMENTS

```

RESULT 1
ID C1W2_HUMAN STANDARD: PRT; 426 AA.
AC 095069; 09UNE3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Potassium channel subfamily K member 2 (Outward rectifying potassium
DE channel protein TREK-1) (TREK-1 K+ channel subunit) (Two-pore
DE potassium channel TPCK1).
GN KCNK2 OR TREK1 OR TREK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=99254549; PubMed=10321245;
RX Patel A.J., Honore F., Leesage F., Fink M., Romey G., Lazdunski M.;
RT "Inhalational anesthetics activate two-pore-domain background K+
RT channels.";
RL Nat. Neurosci. 2:422-426(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Price L.A., Hellings S.E., Hayashi J.H., Pausch M.H.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.
CC -1- SUBUNIT: Homodimer (Potential).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- MISCELLANEOUS: ACTIVATED BY VOLATILE GENERAL ANAESTHETICS SUCH AS
CC CHLOROFORM, HALOTHANE AND ISOFURANE.
CC -1- SIMILARITY: Belongs to the two pore domain potassium channel
CC family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF129399; AAD47569.1; -
CC EMBL: AF004711; AAD01203.1; -
CC Genew, HGNC:6277; KCNK2.
CC MIM: 603219; -
CC GO: GO:0016020; C:membrane; NAS.
CC GO: GO:0015271; F:outward rectifier potassium channel activity; NAS.
CC GO: GO:0006813; P:potassium ion transport; NAS.
CC InterPro: IPR003280; K-channel 2pore.
CC InterPro: IPR001622; K-channel pore.
CC InterPro: IPR003976; Trek channel.
CC PRINTS: PR01333; 2PORECHANNEL.
CC PRINTS: PR01499; TREKCHANNEL.
CC Transport; Ion transport; Ionic channel; Voltage-gated channel;
KW

```

KM Potassium channel; Potassium; Transmembrane; Glycoprotein.  
 FT DOMAIN 1 61  
 FT TRANSSEM 62 82  
 FT TRANSSEM 144 170  
 FT TRANSSEM 172 192  
 FT TRANSSEM 193 223  
 FT TRANSSEM 224 244  
 FT TRANSSEM 253 283  
 FT TRANSSEM 288 308  
 FT DOMAIN 309 426  
 FT DOMAIN 378 426  
 FT DOMAIN 354 426  
 FT CARBOHYD 110 110  
 FT CARBOHYD 134 134  
 FT CONFLICT 2 16  
 FT CONFLICT 309 311  
 FT CONFLICT 391 391  
 FT CONFLICT 411 411  
 SQ SEQUENCE 426 AA; 47016 MW; 2A8A2336D409F4E CRC64;

Query Match 98.4%; Score 2065; DB 1; Length 426;  
 Best Local Similarity 98.8%; Pred. No. 1,4e-136;  
 Matches 406; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MAAPDLDPKSAQNSKRLSPSTKPTVLASRVESDTINWKMKTSTIFLVVLYLI 60  
 DB 16 VAAPDLDPKSAQNSKRLSPSTKPTVLASRVESDTINWKMKTSTIFLVVLYLI 75  
 QY 61 GATVEFALBOPHEISRTTIVIOKOTFISCHSCNSTEDELICQIVAINAGIIPANT 120  
 DB 76 GATVEFALBOPHEISRTTIVIOKOTFISCHSCNSTEDELICQIVAINAGIIPANT 135  
 QY 121 SNQISHMDLGSFFAGVITITIGFNGISPRTEGKFCIIVALLGIPFGFLLAGVDQ 180  
 DB 136 SNQISHMDLGSFFAGVITITIGFNGISPRTEGKFCIIVALLGIPFGFLLAGVDQ 195  
 QY 181 LGTFPKGIAKVBETIKNNVSQTKRIITIIIFLFGCVLFAVPAIIFKHIEGMSLD 240  
 DB 196 LGTFPKGIAKVBETIKNNVSQTKRIITIIIFLFGCVLFAVPAIIFKHIEGMSLD 255  
 QY 241 AIFVAVITITITIGFNGVYAGSDIEFLDFKPVWFMIIVGLAFVAVLMTIGDLRVIS 300  
 DB 256 AIFVAVITITITIGFNGVYAGSDIEFLDFKPVWFMIIVGLAFVAVLMTIGDLRVIS 315  
 QY 301 KKTKEVGEFRAHAEMTAVTAERKTRRLSVIYDKFORATSIKKTLSAELAGNNQ 360  
 DB 316 KKTKEVGEFRAHAEMTAVTAERKTRRLSVIYDKFORATSIKKTLSAELAGNNQ 375  
 QY 361 ELTPCRRLSYVNHLSERDVLPLKTSISYINGLTPHCAGEIIVINIK 411  
 DB 376 ELTPCRRLSYVNHLSERDVLPLKTSISYINGLTPHCAGEIIVINIK 426

RESULT 2  
 C1W2 MOUSE STANDARD; PRT: 411 AA.  
 AC P97438;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Potassium channel subfamily K member 2 (Outward rectifying potassium channel protein TREK-1) (Two-pore potassium channel 1PKC1) (TREK-1 K+ channel subunit).  
 GN KCM2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.  
 RC TISSUE=Brain;

RX MEDLINE=97157476; PubMed=9003761;  
 RA Fink M., Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C.,  
 RA Lazdunski M.,  
 RT "Cloning, functional expression and brain localization of a novel  
 RT unconventional outward rectifier K+ channel.",  
 RL EMBO J. 15:6854-6862(1996).  
 RN [2]  
 RP REVISIONS.  
 RC TISSUE=Brain;  
 RA Fink M., Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C.,  
 RA Lazdunski M.,  
 RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP ACTIVATION.  
 RX MEDLINE=99254548; PubMed=10321245;  
 RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.,  
 RT "Inhalational anesthetics activate two-pore-domain background K+  
 RT channels.",  
 RL Nat. Neurosci. 2:422-426(1999).  
 CC -1- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.  
 CC -1- SUBUNIT: Homodimer (potential).  
 CC -1- TISSUE SPECIFICITY: HIGH EXPRESSION IN BRAIN AND LUNG. ALSO  
 CC DETECTED IN KIDNEY, HEART AND SKELETAL MUSCLE. NOT DETECTED IN  
 CC LIVER, IN THE BRAIN, HIGHEST EXPRESSION IN OLFACTORY BULB,  
 CC HIPPOCAMPUS AND CEREBELLUM.  
 CC -1- MISCELLANEOUS: INHIBITED BY BARIUM. ACTIVATED BY VOLATILE GENERAL  
 CC ANAESTHETICS SUCH AS CHLOROFORM, DIETHYL ETHER, HALOTHANE AND  
 CC ISOFLURANE.  
 CC -1- SIMILARITY: Belongs to the two pore domain potassium channel  
 CC family.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC DR EMBL; U73488; AAC53005.2; -.  
 DR MGD; MGI:109366; Kcm2.  
 DR GO; GO:0008076; C:Voltage-gated potassium channel complex; IDA.  
 DR GO; GO:0005249; F:Voltage-gated potassium channel activity; IDA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . IDA.  
 DR GO; GO:0006813; P:potassium ion transport; IDA.  
 DR InterPro; IPR003280; K+channel\_2pore.  
 DR InterPro; IPR001622; K+channel\_pore.  
 DR InterPro; IPR003976; Trek channel.  
 DR PRINTS: PR01333; 2PORECHANNEL.  
 DR PRINTS: PR01499; TREKCHANNEL.  
 KM Transport; Ion transport; Ionic channel; Voltage-gated channel;  
 KM Potassium channel; Potassium; Transmembrane; Glycoprotein.  
 FT DOMAIN 1 46  
 FT TRANSSEM 47 67  
 FT TRANSSEM 129 155  
 FT TRANSSEM 157 177  
 FT TRANSSEM 178 207  
 FT TRANSSEM 208 228  
 FT TRANSSEM 238 268  
 FT TRANSSEM 273 293  
 FT TRANSSEM 294 411  
 FT DOMAIN 378 411  
 FT CARBOHYD 354 411  
 FT CARBOHYD 95 95  
 FT CARBOHYD 119 119  
 SQ SEQUENCE 411 AA; 45297 MW; 8F976DD103EFA05 CRC64;

Query Match 97.4%; Score 2044; DB 1; Length 411;  
 Best Local Similarity 96.4%; Pred. No. 4e-135;  
 Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

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QY 1 MAAPDLDPKSAQAQNSKPRLSFSTKPTVLASRVESDPTTNMKMKTVSTIFLVVLYLI 60
DB 1 MAAPDLDPKSAQAQNSKPRLSFSTKPTVLASRVESDPTTNMKMKTVSTIFLVVLYLI 60
QY 61 GATVFCALPEPHEISQRTTIVIOKQTFISQHSQVNSTEIDELIQIIVAINAGIPLANT 120
DB 61 GAATVFCALPEPHEISQRTTIVIOKQTFISQHSQVNSTEIDELIQIIVAINAGIPLANT 120
QY 121 SNOISHMDIGSSFFPAGTITTTGFGNISPRTEGGIFCIIYALGIPFPGFLAGVQDQ 180
DB 121 SNOISHMDIGSSFFPAGTITTTGFGNISPRTEGGIFCIIYALGIPFPGFLAGVQDQ 180
QY 181 LGTIFGKGIKAVKEDTPIKNNVSGTKRIIISTIFILFGCVLPAVIFKAIIEGMSALD 240
DB 181 LGTIFGKGIKAVKEDTPIKNNVSGTKRIIISTIFILFGCVLPAVIFKAIIEGMSALD 240
QY 241 AIVFVITLTITGFGDYVAGGSDIEYLDYKPVVWMLVGLAFAVLSMTGMDLRVYS 300
DB 241 AIVFVITLTITGFGDYVAGGSDIEYLDYKPVVWMLVGLAFAVLSMTGMDLRVYS 300
QY 301 KKTKEVGEFRAAFAAMTANVTAEFKETRRRLSVEIYDFORATSIKRLSALAGNNO 360
DB 301 KKTKEVGEFRAAFAAMTANVTAEFKETRRRLSVEIYDFORATSIKRLSALAGNNO 360
QY 361 ELTPCRRITLVNHLTSEBDVLPPLKTESIYANGLTPEAGBIAVENIK 411
DB 361 ELTPCRRITLVNHLTSEBDVLPPLKTESIYANGLTPEAGBIAVENIK 411
RESULT 3
C1WA_RAT STANDARD; PRT; 538 AA.
ID C1WA_RAT STANDARD; PRT; 538 AA.
AC Q9J1S4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE Potassium channel subfamily K member 10 (Outward, rectifying potassium
channel protein TREK-2) (TREK-2 K+ channel subunit).
GN KCKN10 OR TREK2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
NCBI_TaxID=10116;
RX MEDLINE=2029807; PubMed=10747911;
RA Bang H., Kim Y., Kim D.;
RT "TREK-2, a new member of the mechanosensitive tandem-pore K+ channel
family."
RT J. Biol. Chem. 275:17412-17419(2000).
CC -1- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL. PRODUCES RAPIDLY
ACTIVATING AND NON-INACTIVATING OUTWARD RECTIFIER K(+) CURRENTS.
CC ACTIVATED BY ACACIDIC ACID AND OTHER NATURAL OCCURRING.
CC UNSATURATED FREE FATTY ACIDS.
CC SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: EXPRESSED MAINLY IN THE CEREBELLUM, SPLEEN,
AND TESTIS.
CC -1- SIMILARITY: Belongs to the two pore domain potassium channel
family.
CC -----
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CC -----
DR EMBL; AF196965; AAF75132.1;
DR InterPro; IPR003280; K-channel_2pore.
DR InterPro; IPR001622; K-channel_pore.
DR InterPro; IPR003976; Trek_channel.
DR PRINTS; PRO1333; 2PORECHANNEL.

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DR PRINTS; PRO1499; TREKCHANNEL.
KW Transport; Ion transport; Ionic channel; Voltage-gated channel;
KW Potassium channel; Potassium; Transmembrane; Glycoprotein.
FT DOMAIN 1 71
FT TRANSSEM 72 92
FT DOMAIN 154 180
FT TRANSSEM 182 202
FT DOMAIN 203 233
FT TRANSSEM 234 254
FT DOMAIN 263 294
FT TRANSSEM 299 319
FT DOMAIN 320 338
FT CARBOHYD 144 144
FT CARBOHYD 147 147
SQ SEQUENCE 538 AA; 59800 MW; 1FF33F0A52B97E4 CRC64;
Query Match 59.5%; Score 1248.5; DB 1; Length 538;
Beet local similarity 64.6%; Pred. No. 1.1e-79; Indels 11; Gaps 5;
Matches 244; Conservative 58; Mismatches 65;
QY 2 AAPPDLDPKSA--AQNPKPRLSFSTKPTVLASRVESDPT--TTNMKMKTVSTIFLVVYL 56
DB 23 AAPVQCQPKSATNGHHVPRLSISSRATVVA-RMEGASQSGGLQVWKMKTVVAIFVVVVV 81
QY 57 YLTIGATVFCALPEPHEISQRTTIVIOKQTFISQHSQVNSTEIDELIQIIVAINAGIIP 116
DB 82 YLVGVGIVFRLBEPFPSSQNTTALKAFLRDHICVSPQDELTLIQHALDMDNAGVSP 141
QY 117 LGNTSNOISHMDIGSSFFPAGTITTTGFGNISPRTEGGIFCIIYALGIPFPGFLAG 176
DB 142 VGNSNSGSHMDLSAFAFPAGTITTTGFGNISPRTEGGIFCIIYALGIPFPGFLAG 201
QY 177 VGDLGTFGKGIKAVKEDTPIKNNVSGTKRIIISTIFILFGCVLPAVIFKAIIEG 236
DB 202 IGDGLGTFGKGIKAVKEDTPIKNNVSGTKRIIISTIFILFGCVLPAVIFKAIIEG 261
QY 227 SALDAIVFVITLTITGFGDYVAGGSDIEYLDYKPVVWMLVGLAFAVLSMTGMD 295
DB 262 TALESTIFVAVVTLTITGFGDYVAGGSDIEYLDYKPVVWMLVGLAFAVLSMTGMD 321
QY 296 LRVISKKTKEVGEFRAAFAAMTANVTAEFKETRRRLSVEIYDFORATSI---KRLS 351
DB 322 LRVISKKTKEVGEFRAAFAAMTANVTAEFKETRRRLSVEIYDFORATSI---KRLS 381
QY 352 AELAGNHNQELTPCRRITL 369
DB 382 LDORAHSLDMLSPKRSV 399
RESULT 4
C1WA_HUMAN STANDARD; PRT; 538 AA.
ID C1WA_HUMAN STANDARD; PRT; 538 AA.
AC P57789; Q8TDK7; Q8TDK8; Q9HB59;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE Potassium channel subfamily K member 10 (Outward, rectifying potassium
channel protein TREK-2) (TREK-2 K+ channel subunit).
GN KCKN10 OR TREK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RX MEDLINE=20435789; PubMed=10880510;
RA Lesage F., Terrenoire C., Romey G., Lazdunski M.;
RT "Human TREK2, a 2P domain mechanosensitive K+ channel with multiple
RT G1 and Gq protein-coupled receptors."
RT J. Biol. Chem. 275:28398-28405 (2000).
RN [2]
RX SEQUENCE FROM N.A. (ISOFORMS B AND C).

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[illegible]

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RT "Cloning of two transcripts, HKT4.1a and HKT4.1b, from the human
RT two-pore K+ channel gene KCNKA. Chromosomal localization, tissue
RT distribution and functional expression."
RT Brain Res. Mol. Brain Res. 102:18-27(2002).
CC -1- FUNCTION: VOLTAGE INSENSITIVE, INSTANTANEOUS, OUTWARDLY RECTIFYING
CC POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS REVERSED AT HIGH
CC EXTERNAL K+ CONCENTRATIONS (BY SIMILARITY).
CC -1- SUBUNIT: Homodimer (Potential).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Kt4.1a;
CC IsoId=Q9NYG8-1; Sequence=Displayed;
CC Name=2; Synonyms=Kt4.1b;
CC IsoId=Q9NYG8-2; Sequence=VSP_006689;
CC -1- SIMILARITY: Belongs to the two pore domain potassium channel
CC family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF248242; AACG31731.1; -.
CC EMBL; AF247042; AAF64062.1; ALT_INIT.
CC EMBL; AF259500; AAK49389.1; -.
CC EMBL; AF259501; AAK49390.1; -.
CC GeneW; HGNC:6279; KCNKA.
CC MIM; 605720; -.
CC GO; GO:0005267; F:potassium channel activity; TMS.
CC GO; GO:0006813; P:potassium ion transport; TMS.
CC InterPro; IPR003280; K+channel_2pore.
CC InterPro; IPR001622; K+channel_pore.
CC InterPro; IPR008074; TRAAK channel.
CC PRINTS; PR01333; 2PORECHANNEL.
CC TRINETS; PR01691; TRAAKCHANNEL.
CC K+ transport; Ion transport; Ionic channel; Voltage-gated channel;
CC Potassium channel; Potassium; Transmembrane; Glycoprotein;
CC Alternative splicing.
CC FT DOMAIN 1 3 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 4 24 PORE-FORMING 1 (POTENTIAL).
CC FT TRANSMEM 89 113 PORE-FORMING 1 (POTENTIAL).
CC FT TRANSMEM 118 138 POTENTIAL.
CC FT TRANSMEM 139 171 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 172 192 POTENTIAL.
CC FT DOMAIN 197 221 PORE-FORMING 2 (POTENTIAL).
CC FT TRANSMEM 234 254 POTENTIAL.
CC FT DOMAIN 255 393 CYTOPLASMIC (POTENTIAL).
CC CARBOHYD 78 78 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC VARSPPLIC 1 1 M -> MTAPOEPPAPPLAGSGAGPAPGRAM (in
CC isoform 2).
CC /FTID=VSP_006689.
CC FT CONFLICT 328 328 F -> L (IN REF. 2).
CC SQ SEQUENCE 393 AA; 42704 MW; 7F18E53A0A9AD57D CRC64;
Query Match 38.3%; Score 803; DB 1; Length 393;
Best Local Similarity 51.1%; Pred. No. 7.6e-49;
Matches 145; Conservative 61; Mismatches 76; Indels 2; Gaps 1;

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Db 121 IFVALVGIPLFGILLAGVGRDLGSSLRHGHIEAIFLKNHVPPELVRLVSLMLFLIGC 180
Qy 220 VLFPALPPIIRKHIEGMSALDAIFVYITLTITFGDGYVAGSGIETLDFKPYVWIL 279
Db 181 LFLVLTPTFVFCYEDMSKEAIFVITVITVTFVFGYVAGADPROSPAYQPLWFWIL 240
Qy 280 VGLAFPAVLMEIDMLRVISKRTKEVEGFRAAEWTAVTA 323
Db 241 LGIAVFASVLTITGMRLRVSRRTRAEMGULTAQAASMTGVTA 264

RESULT 6
ID C1W4 MOUSE STANDARD; PRT; 398 AA.
AC 088454;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Potassium channel subfamily K member 4 (TRAK-related arachidonic acid-
DE stimulated potassium channel protein) (TRAK).
GN KCNKA OR TRAK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
(1)
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98292450; PubMed=9628867;
RA Fink M., Lesage F., Duprat F., Heurteaux C., Reyes R., Fosset M.,
RA Lazdunski M.,
RT "A neuronal two P domain K+ channel stimulated by arachidonic acid and
RT polyunsaturated fatty acids."
RL EMBO J. 17:3297-3308(1998).
[2]
RP ACTIVATION.
RX MEDLINE=99254548; PubMed=10321245;
RA Patel A.U., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
RT "Inhalational anesthetics activate two-pore-domain background K+
RT channels."
RL Nat. Neurosci. 2:422-426(1999).
CC -1- FUNCTION: VOLTAGE INSENSITIVE, INSTANTANEOUS, OUTWARDLY RECTIFYING
CC POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS REVERSED AT HIGH
CC EXTERNAL K+ CONCENTRATIONS.
CC -1- SUBUNIT: Homodimer (Potential).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=088454-1; Sequence=Displayed;
CC Name=2; Synonyms=TRAKT, Truncated;
CC IsoId=088454-2; Sequence=VSP_006690, VSP_006691;
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SPINAL CORD AND EYE. NOT
CC DETECTED IN HEART, SKELETAL MUSCLE, LIVER, LUNGS, KIDNEY AND
CC TESTIS.
CC -1- MISCELLANEOUS: ACTIVATED BY ARACHIDONIC ACID AND OTHER UNSATURATED
CC FATTY ACIDS. NOT AFFECTED BY VOLATILE GENERAL ANAESTHETICS SUCH AS
CC CHLOROFORM, DIETHYL ETHER, HALOTHANE AND ISOFURANE.
CC -1- SIMILARITY: Belongs to the two pore domain potassium channel
CC family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF056492; AAC40181.1; -.
CC MGD; MGI:1298234; Kcnk4.
CC InterPro; IPR003280; K+channel_2pore.
CC InterPro; IPR001622; K+channel_pore.

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DR InterPro: IPR008074; TRAAK_channel.
DR PRINTS: PR01333; 2PORECHANNEL.
DR PRINTS: PR01691; TRAAKCHANNEL.
DR Transport; Ion transport; Ionic channel; Voltage-gated channel;
KM Potassium channel; Potassium; Transmembrane; Glycoprotein;
KM Alternative splicing.
FT DOMAIN 1 3
FT TRANSMEM 4 24
FT DOMAIN 89 113
FT TRANSMEM 119 139
FT DOMAIN 140 171
FT TRANSMEM 172 192
FT DOMAIN 198 222
FT TRANSMEM 235 255
FT DOMAIN 256 398
FT CARBOHYD 81 81
FT CARBOHYD 84 84
FT VARSPIC 63 67
FT VARSPIC 68 398
FT VARSPIC 68 398
SQ SEQUENCE 398 AA; 43051 MW; 478A834B7B7AE92 CRC64;
Query Match 37.0%; Score 776.5; DB 1; Length 398;
Best Local Similarity 49.8%; Pred. No. 5,3e-47;
Matches 142; Conservative 57; Mismatches 83; Indels 3; Gaps 1;
QY 42 MKKKVSTFLVYVLLIGATVFKALQPHISQRTTIVIKQFISGHSVNSTELDE 101
DB 1 MKRTLLALLALLVLLVSGALVQLQEPHQKQKRRDQFLRDHPVCSKSLSD 60
QY 102 LKQIVAAINAGIIP--LGNTSNQISHWDLGSSFFAGTAVTTTIGFNGISPRTEGKIF 158
DB 61 FILVLEALGGGANPETSMTNSNSANLGSAPFSGTITTTIGYGNIVHTDARLF 120
QY 159 CIYVALGIPURFLLAGVGDQGTGKGIKVEDTPIKKNVSGTKRIISTITFIIFG 218
DB 121 CIFVALVGLPLFEMLAGVDRIGSSLRGIGHIEFLKHPVPGIVRSLSAVLFLIG 180
QY 219 CVLFVALPAIIFKHIGMGALDAIVYVTTTIGFGDVAGSGSIEYDFKPVWPMI 278
DB 181 CLIFVLTFFVFSYMSKSKLEALIVYVTLTTFVGDFVDPDGGQNSPAQPLVWMI 240
QY 279 LVGLAVFAVLNIGDWLRVISKTKKEVGFRAHAEWTANVTA 323
DB 241 LFLGLAVFASVLTITIGNWLRAVSRRTAEWEGGLTAQASWTGTVTA 285
RESULT 7
CING_HUMAN STANDARD; PRT; 309 AA.
ID CING_HUMAN STANDARD; PRT; 309 AA.
AC Q96T55; Q9H591;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Potassium channel subfamily K member 16 (TWIK-related alkaline pH
DE activated K+ channel 1) (2p domain potassium channel Taik-1).
GN KCKN16 OR TALK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Pancreas;
RX MEDLINE=21164727; PubMed=11263999;
RA Girard C., Duprat F., Terrenoire C., Tinel N., Fosset M., Romey G.,
RA Lazdunski M., Lesage F.,
RT "Genomic and functional characteristics of novel human pancreatic 2p
RT domain K(+) channels.";
RU Biochem. Biophys. Res. Commun. 282:249-256(2001).
RN [2]
SQ SEQUENCE FROM N.A. (ISOFORM 2).

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RA Williams S.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Outward rectifying potassium channel. Produces rapidly
CC activating and non-inactivating outward rectifier K(+) currents.
CC -1- SUBUNIT: Homodimer (Potential).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q96T55-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q96T55-2; Sequence=VSP_006699;
CC Note=No experimental confirmation available;
CC -1- TISSUE SPECIFICITY: Highly expressed in pancreas. Not detectable
CC in the other tissues tested.
CC -1- MISCELLANEOUS: Inhibited by Ba(+2), guanine, quinidine, chloroform
CC and halothane. Activated at alkaline pH.
CC -1- SIMILARITY: Belongs to the two pore domain potassium channel
CC family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF358809; AK49532.1; -
DR EMBL: AL136087; CAC07336.1; -
DR Genew: HGNC:14464; KCKN16.
DR MIM: 607369; -
DR InterPro: IPR003280; K+channel 2pore.
DR InterPro: IPR001622; K+channel pore.
DR InterPro: IPR003092; TASK channel.
DR PRINTS: PR01333; 2PORECHANNEL.
DR PRINTS: PR01095; TASKCHANNEL.
DR Transport; Ion transport; Ionic channel; Voltage-gated channel;
KM Potassium channel; Potassium; Transmembrane; Alternative splicing.
FT DOMAIN 1 13
FT TRANSMEM 14 34
FT DOMAIN 98 116
FT TRANSMEM 120 140
FT DOMAIN 141 165
FT TRANSMEM 166 186
FT DOMAIN 202 221
FT TRANSMEM 238 258
FT DOMAIN 259 309
FT VARSPIC 269 309
FT VARSPIC 269 309
FT VARSPIC 269 309
SQ SEQUENCE 309 AA; 34153 MW; 99C4B11EB26B0764 CRC64;
Query Match 24.0%; Score 502.5; DB 1; Length 309;
Best Local Similarity 39.0%; Pred. No. 4,6e-28;
Matches 97; Conservative 56; Mismatches 83; Indels 13; Gaps 5;
QY 47 VSTIFLVVLLIGATVFKALQPHISQRTTIVIKQFISGHSVNSTELDIQOI 106
DB 14 VLPELLAVCYVLLIGATIFOLLERQAQSRQFQLEKRLFLENYTCIDQMAWEGVQYI 73
QY 107 VAAINAGIIPGNTSNQISHWDLGSSFFAGTAVTTTIGFNGISPRTEGKICITIAIG 166
DB 74 MEAWKGVNPKGSTNP-SNWDGSSFFAGTAVTTTIGFNGISPRTEGKICITIAIG 132
QY 167 IPLFGLLAGVGDQGTGKGIKVEDTPIKKNVSGTKRIISTITFIIFGCVLEV 223
DB 133 IPLNVLEF---NHLTGRLRAHLAIE---RWEDRRSSQVLQVGLALFTLGLTVIL 184
QY 224 ALPAIIFKHIGMSALDAIVYVTTTIGFGDVAGSGDIE-YLDFYKPVWPMIYV 282
DB 185 IFPPWFSHVEGWSFSEGFYFATITSTIGFDGVVGTDPKRTISVYSLAAIWLGL 244

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QY 283 AYPAAVLSM 291  
 DB 245 AMLATLPL 253

## RESULT 8

C1W5\_HUMAN STANDARD; PRT; 499 AA.  
 AC 095273;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Potassium channel subfamily K member 5 (Acid-sensitive potassium channel protein TASK-2) (TWIK-related acid-sensitive K<sup>+</sup> channel 2).  
 GN KCNK5 OR TASK2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=99030343; PubMed=9812978;  
 RA Reyes R., Duprat F., Lesage F., Fink M., Salinas M., Farman N., Lazdunski M.;  
 RT "Cloning and expression of a novel pH-sensitive two pore domain K<sup>+</sup> channel from human kidney."  
 RL J. Biol. Chem. 273:30863-30869(1998).  
 CC -1- FUNCTION: PH DEPENDENT, VOLTAGE INSENSITIVE, OUTWARDLY RECTIFYING POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS LOST AT HIGH EXTERNAL K<sup>+</sup> CONCENTRATIONS.  
 CC -1- SUBUNIT: Homodimer (Potential).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -1- TISSUE SPECIFICITY: ABUNDANT EXPRESSION IN KIDNEY, ALSO DETECTED IN LIVER, PLACENTA AND SMALL INTESTINE. IN THE KIDNEY, EXPRESSION IS RESTRICTED TO THE DISTAL TUBULES OR GLOMERULI.  
 CC -1- EXPRESSED IN PROXIMAL TUBULES OR GLOMERULI.  
 CC -1- MISCELLANEOUS: INHIBITED BY QUININE, QUINIDINE AND EXTERNAL ACIDIFICATION.  
 CC -1- SIMILARITY: Belongs to the two pore domain potassium channel family.  
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 CC -----  
 DR EMBL; AF084830; AAC79458.1; -.  
 DR Genew; HGNC:6280; KCNK5.  
 DR MIM; 603493; -.  
 DR GO; GO:0005887; C: integral to plasma membrane; TAS.  
 DR GO; GO:0005267; F: potassium channel activity; TAS.  
 DR GO; GO:0007588; P: excretion; TAS.  
 DR GO; GO:000613; P: potassium ion transport; TAS.  
 DR InterPro; IPR003280; K+channel\_2pore.  
 DR InterPro; IPR001622; K+channel\_pore.  
 DR InterPro; IPR003092; TASK channel.  
 DR PRINTS; PR01333; 2PORECHANNEL.  
 DR PRINTS; PR01095; TASKCHANNEL.  
 DR Transport; Ion transport; Ionic channel; Voltage-gated channel;  
 KM Potassium channel; Potassium; Transmembrane; Glycoprotein.  
 FT DOMAIN 1  
 FT TRANSMEM 7  
 FT TRANSMEM 8 26  
 FT TRANSMEM 85 112 PORE-FORMING 1 (POTENTIAL).  
 FT TRANSMEM 113 133 POTENTIAL.  
 FT TRANSMEM 134 157 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 158 180 POTENTIAL.  
 FT DOMAIN 190 215 PORE-FORMING 2 (POTENTIAL).  
 FT TRANSMEM 230 250 POTENTIAL.

FT DOMAIN 251 325 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 77 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 499 AA; 55130 MW; E871A7A482DDA00 CRC64;

Query Match 20.5%; Score 430; DB 1; Length 499;  
 Best local similarity 31.1%; Pred. No. 8,4e-23;  
 Matches 106; Conservativity 61; Mismatches 120; Indels 54; Gaps 11;

QY 54 VVLLIIGATVPKALKEPHISORTTIVIGKQFPIGSHSCVSNSTDELIIQGVAAINAG 113  
 DB 12 IIFYLAIQPAIFWELEBPHWKAKNYTQKHLKEFFPLGDEGDKILFVVSDAAGG 71  
 QY 114 IIPKGNSTNOISHVLDSSFFPAGVITTTIGPNISIRTEGKIFCIYIALGIPLRGL 173  
 DB 72 VALIGNQT--FNNMWNPMIPATVITTTIGGVNAKPTAGRLFCVYGLFGVPL---C 126  
 QY 174 LAGVDDLGITTFGKIAKVEDTPIKMNVSQTKRIITITFIPLFGCVLPALALIFKH 233  
 DB 127 LTVI-SALGKFFGGARARLQFLTKRGVSLRKAQITCTVIFIVGVLVHLVIPPVMT 185  
 QY 234 EGWGLDAIYFVVTITTTIGFGDYVAG-GSDIEYDFKPVWFWIIVGLAYPEAVLSMT 292  
 DB 186 EGVYIIEGLYVSFTTITTTIGFGDYVAGVSNPANYHALYRFVLMYIGLAW---LSLF 241  
 QY 293 GDWIRVTSKTKREVEGFRAHAEWTVANTVAERKTRRLSVETIDYKQATSIKKLSA 352  
 DB 242 VNW-----KVSWF-----VEVHKAIKKRRR-----RKESF 267  
 QY 353 ELAGNHQELPCCRITSVNHLISRPV--LPPLTKRESY 391  
 DB 268 E-SSEHS-----RKALQVKGSTASKDVNIFFLSKEEY 301

## RESULT 9

C1W6\_HUMAN STANDARD; PRT; 332 AA.  
 AC 096T54; Q8TAM4; Q9BXD1; Q9H592;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Potassium channel subfamily K member 17 (TWIK-related alkaline pH activated K<sup>+</sup> channel 2) (2P domain potassium channel Talk-2) (TWIK-related acid-sensitive K<sup>+</sup> channel 4) (TASK-4).  
 GN KCNK17 OR TALK2 OR TASK4.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Pancreas;  
 RX MEDLINE=21164727; PubMed=11263999;  
 RA Girard C., Duprat F., Terrenoire C., Tinel N., Fosset M., Romey G., Lazdunski M., Lesage F.;  
 RT "Genomic and functional characteristics of novel human pancreatic 2P domain K<sup>+</sup> channels."  
 RL Biochem. Biophys. Res. Commun. 282:249-256(2001).  
 RN [2]  
 RN SEQUENCE FROM N.A. (ISOFORM 2).  
 RP TISSUE=Adrenal gland;  
 RX MEDLINE=21145510; PubMed=11248242;  
 RA Decher N., Maier M., Dietrich W., Gassenhuber J., Brueggemann A., Busch A.E., Steinmeyer K.;  
 RT "Characterization of TASK-4, a novel member of the pH-sensitive, two-pore domain potassium channel family."  
 RL FEBS Lett. 492:84-89(2001).  
 RN [3]  
 RN SEQUENCE FROM N.A. (ISOFORM 1).  
 RA Williams S.;  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Lung, and Spleen;



RX MEDLINE=22388257; PubMed=12477932;  
 RA Krausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Altschul S., Collins F.S., Wagner L., Shellen G.M., Schuler G.D.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Datchenko J., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Pange C.,  
 RA Raha S.S., Loughlano N.A., Peters G.J., Abramson R.D., Mullish S.U.,  
 RA Bosak S.A., McMan P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Scheraga A., Schein U.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: Outward rectifying potassium channel. Produces rapidly  
 activating and non-inactivating outward rectifier K(+) currents.  
 CC -1- SUBUNIT: Homodimer (potential).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=Q96T54-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=Q96T54-2; Sequence=VSP\_006700;  
 CC Note=No experimental confirmation available;  
 CC MISCELLANEOUS: Inhibited by Ba(2+), quinidine, chloroform and  
 halothane. Activated at alkaline pH. Activated by guanine and  
 isoflurane.  
 CC -1- SIMILARITY: Belongs to the two pore domain potassium channel  
 family.  
 CC -1- CAUTION: Ref.3 sequence differs from that shown due to erroneous  
 gene model prediction.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; AF358910; AAK49533.1; -;  
 DR EMBL; AF339912; AAK28551.1; -;  
 DR EMBL; AL136087; CAC07335.1; ALT\_SEQ.  
 DR EMBL; BC025726; AAK25726.1; -;  
 DR GeneW; HGNC:14465; KCNK17.  
 DR MIM; 607370; -;  
 DR InterPro; IPR003280; K+channel\_2pore.  
 DR InterPro; IPR001622; K+channel\_pore.  
 DR InterPro; IPR003092; TASK channel.  
 DR PRINTS; PRO1333; 2PORECHANEL.  
 DR PRINTS; PRO1095; TASKCHANNEL.  
 KW Transport; Ion transport; Ionic channel; Voltage-gated channel;  
 KW Potassium channel; Potassium; Transmembrane; Glycoprotein;  
 KW Alternative splicing.  
 FT DOMAIN 1 20  
 FT TRANSMEM 21 43 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 106 124 POTENTIAL.  
 FT TRANSMEM 128 148 PORE-FORMING 1 (POTENTIAL).  
 FT DOMAIN 149 179 POTENTIAL.  
 FT TRANSMEM 180 200 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 211 230 POTENTIAL.  
 FT TRANSMEM 244 264 PORE-FORMING 2 (POTENTIAL).  
 FT DOMAIN 265 332 POTENTIAL.  
 FT CAROXYD 65 65 CYTOPLASMIC (POTENTIAL).  
 FT CAROXYD 94 94 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROXYD 94 94 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT VARSPLIC 260 332 IKLLISQLEPRGVSCCHSSKEDPKSQRWDPPRPS  
 FT HSPQGGYPPGPGGIIIOHLEPRSAHAGCGDS -> SNSS  
 FT PSMRQGGYPPAATLALRRTSSPKADRLTQSGPTPSK  
 FT DATORDPWSYSIMNLLTLQAIVARTASTYPPGRRPR  
 FT (in isoform 2).  
 FT /Frid=vsp\_006700.  
 FT S -> G (IN REF. 2 AND 4).  
 FT SEQUENCE 332 AA; 36894 MW; 1648DBC06E78158 CRC64;  
 SO  
 Query Match 18.7%; Score 393; DB 1; Length 332;  
 Best Local Similarity 36.1%; Pred. No. 2e-20;  
 Matches 91; Conservative 53; Mismatches 92; Indels 16; Gaps 7;  
 QY 48 STFLVY--LVYLLIGATVKAEGHEHSRTIYIQGTFISQSCVNSYELDLIQ 105  
 DB 21 STVLLAVAYALALGCVWTLTEGRAQDSSSPFQDKWELLQNTCLDRPALDLND 80  
 QY 106 IVAAINAGIIPLCNTSNOISHWLGGSPFPAQVITTTIGFNGISPTREGKIPICITALL 165  
 DB 81 VQAVKYGASLLSNTS-MGRWELVGSFPFVSITTTIGVGNLSPVTMARLFCIFPALV 139  
 QY 166 GIPPLFGLAGVGDQCTIFGKGI---AKVETFTKNAVSTKRIITITIFILFGVL 221  
 DB 140 GIPNLVYL---NRGHLWQGVNHWASRLGST--WQ-DPKAKWLAGSGLLSGLL 191  
 QY 222 FVALPAIIFPGHGMGALDAIVFVITLTIGGDIYVAGSDIE-YLDFKXVFWFWILV 280  
 DB 192 FULLPLPLFSHMGWSTEGFYAFITLSTVGGDVIAGNPSQRPFLVYKXVSWILVF 251  
 QY 281 GLAVFAVLSMI 292  
 DB 252 GMAMALLIILKI 263  
 RESULT 10  
 ID CIRM\_HUMAN STANDARD; PRT; 336 AA.  
 AC 000180; Q13307;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Potassium channel subfamily K member 1 (inward rectifying potassium  
 DE channel protein TWIK-1) (Potassium channel KONO1).  
 GN KCNK1 OR TWIK1 OR KONO1 OR KONO1.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., FUNCTION, AND MUTAGENESIS OF THR-161.  
 RC TISSUE=Kidney;  
 RA MEDLINE=96183184; PubMed=8605869;  
 RA Lesage F., Guillemare E., Fink M., Duprat F., Lazdunski M., Romey G.,  
 RA Barhanin J.,  
 RT "TWIK-1, a ubiquitous human weakly inward rectifying K+ channel with a  
 RT novel structure.";  
 RT EMBO J. 15:1004-1011(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND REVIEW.  
 RC TISSUE=Brain;  
 RA MEDLINE=98122696; PubMed=9462864;  
 RA Goldstein S.A.N., Wang X.-W., Ilan N., Pausch M.H.,  
 RT "Sequence and function of the two P domain potassium channels:  
 RT implications of an emerging superfamily.";  
 RT J. Mol. Med. 76:13-20(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=98026667; PubMed=9362344;  
 RA Orlas M., Velazquez H., Tung F., Lee G., Desir G.V.,  
 RT "Cloning and localization of a double-pore K channel, KCNK1: exclusive  
 RT expression in distal nephron segments.";  
 RU Am. J. Physiol. 273:F663-F666(1997).  
 RN [4]



RP SEQUENCE FROM N.A.  
 CC TISSUE=Brain;  
 RX MEDLINE=22386257; PubMed=12477932;  
 RA Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Urdan T.B., Tothyluki S., Carninci P., Parise C.,  
 RA Raha S.S., Longellano N.A., Peters G.J., Abramson R.D., Mallya S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.U., Malek U.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey U., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.T., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein U.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: Weakly inward rectifying potassium channel.  
 CC -1- SUBUNIT: Homodimer (potential).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).  
 CC -1- TISSUE SPECIFICITY: Widely expressed with high levels in heart and  
 CC brain and lower levels in placenta, lung, liver and kidney.  
 CC -1- MISCELLANEOUS: Inhibited by barium, quinine, quinidine and  
 CC internal acidification. Activated by protein kinase C.  
 CC -1- SIMILARITY: Belongs to the two pore domain potassium channel  
 CC family.  
 CC -----  
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 CC -----  
 DR EMBL: U33632; AAB01688.1; -  
 DR EMBL: U76996; AAB97878.1; -  
 DR EMBL: U90065; AAB5147.1; -  
 DR EMBL: BC018051; AAI18051.1; -  
 DR PIR: S65566; S65566.  
 DR GeneW: HGNC:6272; KCNK1.  
 DR MIM: 601745; -  
 DR GO: GO:0008076; C:Voltage-gated potassium channel complex; TNS.  
 DR GO: GO:0005242; F:Inward rectifier potassium channel activity; TNS.  
 DR GO: GO:0006813; P:Potassium ion transport; TNS.  
 DR InterPro: IPR003280; K+channel\_2pore.  
 DR InterPro: IPR001622; K+channel\_pore.  
 DR InterPro: IPR001779; TWIK1\_channel.  
 DR PRINTS: PRO05408; TWIK1\_channel.  
 DR PRINTS: PRO1333; 2PORECHANNEL.  
 DR PRINTS: PRO1096; TWIK1CHANNEL.  
 DR PRINTS: PRO1586; TWIKCHANNEL.  
 KW Transport; Ion transport; Ionic channel; Voltage-gated channel;  
 KW Potassium channel; Potassium; Transmembrane; Glycoprotein.  
 FT DOMAIN 1 20  
 FT TRANSEM 21 41  
 FT DOMAIN 104 130  
 FT TRANSEM 133 153  
 FT DOMAIN 154 177  
 FT TRANSEM 179 198  
 FT DOMAIN 212 238  
 FT TRANSEM 247 267  
 FT DOMAIN 268 336  
 FT TRANSEM 295 315  
 FT CATABOL 336 361  
 FT METAGEN 161 161  
 FT SEQUENCE 336 AA; 38143 MW; 2A41D950132325D CRC64;

Query Match 18.1%; Score 379.5; DB 1; Length 336;  
 Best Local Similarity 32.5%; Pred. No. 1,8e-19;  
 Matches 90; Conservative 62; Mismatches 108; Indels 17; Gaps 9;  
 51 FLVY--VLYLIGATVKALEQPHISQRTTIVQKQTFISQSCVNSTELDELICQIVA 108  
 DB FLVGYLLVYFAGVAVSSVELPEDLLROELRLKRFLEHCHLSQQLQEPVGNVLE 84  
 QY AINAGIPLGNTSQIQSHMDGSSFPFAGVITTTIGGNTSPREGKIPCIYALGIP 168  
 DB ASNVGVSTLSASGN-NMWDPTSLFFASTYLSITGCHVPLSDGKARCIITVSIGIP 143  
 QY 169 LFGFLGAVGQDLGTTEGKIAKVEDTFIKNNVQTKIRIISITII--FILECYLVALP 226  
 DB FTLLFLAVVQRIYVYTR--RPVLYPHIRGFSKQVAVIYHVALGFTVVSCEFFI--P 199  
 QY 227 AIFPKHIE-GMSALDAIYFVITLTITGFGPYVAG-GSDIEYLDYFYPVWFVTLVGLAY 284  
 DB 200 AAVSVLEDDNFFESYFCFISTIGLDYVGGYGNQKFRLLYKIGITCYLLGLIA 259  
 QY 285 FAAYLSMIGDLRVISK----KTKRVEGEFRHAAAE 316  
 DB 260 MLVVLFFCE-LHLLKFRKMFYVKDKDEQVHIE 295  
 RESULT 11  
 ID C1W1 MOUSE STANDARD; PRT; 336 AA.  
 AC 008581;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Potassium channel subfamily K member 1 (inward rectifying potassium  
 DE channel protein TWIK-1).  
 GN GN  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=9716599; PubMed=9013852;  
 RA Lesage F., Lauritzen I., Duprat F., Reyes R., Fink M., Heurteaux C.,  
 RA Lazdunski M.,  
 RT "The structure, function and distribution of the mouse TWIK-1 K+  
 RT channel."  
 RL FEBS Lett. 402:28-32(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SVJ; TISSUE=Liver;  
 RX MEDLINE=98218573; PubMed=9559671;  
 RA Arrighi I., Lesage F., Scimeca U.-C., Carle G.F., Barhanin U.,  
 RT "Structure, chromosome localization, and tissue distribution of the  
 RT mouse twik K+ channel gene."  
 RL FEBS Lett. 425:310-316(1998).  
 CC -1- FUNCTION: Weak inwardly rectifying potassium channel.  
 CC -1- SUBUNIT: Homodimer (potential).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).  
 CC -1- TISSUE SPECIFICITY: Widely expressed. Highest expression in brain,  
 CC kidney, thyroid, salivary gland, adrenal gland, prostate,  
 CC epididymis, uterus, placenta, colon and jejunum. Moderate  
 CC expression in eyes, pituitary, pancreas, smooth muscle, testis and  
 CC ovary. Very low levels in lung, aorta, liver, heart, skeletal  
 CC muscle, thymus and spleen. In the brain, highest expression in  
 CC cerebellar granule cells, brainstem, hippocampus and cerebral  
 CC cortex.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSION DETECTED AS EARLY AS 7 DAYS POST  
 CC CONCEPTION. EXPRESSION INCREASES FROM 2-8 DAYS AFTER BIRTH AND  
 CC STABILIZES AFTER DAY 8.  
 CC -1- MISCELLANEOUS: INHIBITED BY QUININE, BARBIT, AND INTERNAL  
 CC ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C.  
 CC -1- SIMILARITY: Belongs to the two pore domain potassium channel

## family.

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DR EMBL: AF03017; AAC16973.1; -  
DR MGD: MGI:109322; Kcnk1.  
DR InterPro: IPR003280; K+channel\_2pore.  
DR InterPro: IPR001622; K+channel\_pore.  
DR InterPro: IPR001779; TWIK1\_channel.  
DR InterPro: IPR005408; TWIK1\_channel.  
DR PRINTS: PR01333; 2PORECHANNEL.  
DR PRINTS: PR01095; TWIK1CHANNEL.  
DR PRINTS: PR01586; TWIK1CHANNEL.  
KM Transport; Ion transport; Ionic channel; Voltage-gated channel;  
KW Potassium channel; Potassium; Transmembrane; Glycoprotein.  
FT DOMAIN 1 20  
FT TRANSMEM 21 41  
FT DOMAIN 104 130  
FT TRANSMEM 133 153  
FT TRANSMEM 154 177  
FT TRANSMEM 178 198  
FT TRANSMEM 212 238  
FT TRANSMEM 247 267  
FT TRANSMEM 268 336  
FT CARBOHYD 95  
SQ SEQUENCE 336 AA; 38275 MW; A996060A18265FD4 CRC64;

Query Match 17.7%; Score 370.5; DB 1; Length 336;  
Best Local Similarity 33.9%; Pred. No. 7.6e-19;

Matches 83; Conservative 57; Mismatches 94; Indels 11; Gaps 7;

QY 51 FLVW-VLYLIGATVFKALQEPHEISQRTTIVIQKQTFISGSCVNSTELDELIQIVVA 108  
DB 25 FLVGLYGLTVGVAVVFSSEELPYEDLLKQELKRRRLREHECTLSEPOLEQFGRVLE 84  
QY 109 AINAGIPIGNTSNQSHWDLGSSPPFAGTVTTTIGFNGISRTGKIFCIYVLLGIP 168  
DB 85 ASNYGVSVSNASGN-WNWDFTSALFPASTVLTSTGYGTAPLSGGRAFCTISVIGIP 143  
QY 169 LFGFLAGVDQGLTIFGKIAKVEDTFKMNVSQTKIRIISTII--FILFGCVLVALP 226  
DB 144 FTLLFETLVGVTVHVR--RPVLYHIRMGSQVAVYAVLVGVTWSCFFFI--P 199  
QY 227 AITFKATIE-GMSALDAIYFVVTTLTTIGFGDYVAG-GSDIEYLDYKRVVWFWIIVGLAY 284  
DB 200 AAFVSYLEDNMFLESFYFCFSLSTIGLDYVPEGVNOKRRELKIGITCYLLGLIT 259  
QY 285 FAAYL 289  
DB 260 MLVVL 264

RESULT 12

CIT3 HUMAN STANDARD; PRT; 394 AA.  
ID CIT3 HUMAN  
AC 014649;  
DT 16-OCT-2001 (Rel. 40; Last sequence update)  
DT 16-OCT-2001 (Rel. 40; Last annotation update)  
DE 15-MAR-2004 (Rel. 43; Last annotation update)  
DE Potassium channel subfamily K member 3 (Acid-sensitive potassium  
DE channel protein TASK-1) (TWIK-related acid-sensitive K+ channel 1)  
DE (Two pore potassium channel KTR.1).  
GN KONK3 OR TASK1 OR TASK.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;

EN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RX MEDLINE=97459932; PubMed=9312005;  
RA Duprat F., Lesage F., Fink M., Reyes R., Heurteaux C., Lazdunski M.;  
RT "TASK, a human background K+ channel to sense external pH variations  
RT near physiological pH.";  
RL EXPO J. 16:5464-5471(1997).  
EN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Heart;  
RA Lopes C.M.B., Gallagher P.G., Buck M.E., Butler M.H.,  
RA Goldstein S.A.N.;  
RT "Proton block and voltage-gating are potassium-dependent in the  
RT cardiac leak channel Kcnk3.";  
RL Submitted (May-1998) to the EMBL/GenBank/DBJ databases.  
EN [3]  
RP MEDLINE=99254548; PubMed=10321245;  
RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;  
RT "Inhalational anesthetics activate two-pore-domain background K+  
RT channels.";  
RL Nat. Neurosci. 2:422-426(1999).  
EN [4]  
RP MUTAGENESIS OF HIS-98.  
RX MEDLINE=21535313; PubMed=11690614;  
RA Ashmole I., Goodwin P.A., Stanfield P.R.;  
RT "TASK-5, a novel member of the tandem pore K+ channel family.";  
RL Pflügers Arch. 442:828-833(2001).  
CC -1- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM  
CC CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM  
CC ION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN  
CC OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW.  
CC WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -1- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN ADULT. STRONGEST  
CC EXPRESSION IN PANCREAS AND PLACENTA. LOWER EXPRESSION IN BRAIN,  
CC LUNG, PROSTATE, HEART, KIDNEY, UTERUS, SMALL INTESTINE AND COLON.  
CC -1- MISCELLANEOUS: INHIBITED BY EXTERNAL ACIDIFICATION. ACTIVATED BY  
CC HALOTHANE AND ISOFLURANE.  
CC -1- SIMILARITY: Belongs to the two pore domain potassium channel  
CC family.  
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RT (TOSS) : a novel human 2-pore K<sup>+</sup> channel principal subunit." ;  
 RL FEBS Lett. 450:191-196(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND MUTAGENESIS OF CVS-53.  
 RC TISSUE=Brain;  
 RX MEDLINE=99175162; PubMed=10075682;  
 RA Chavez R.A., Gray A.T., Zhao B.B., Kindler C.H., Mazurek M.J.,  
 RT Mehta Y., Forsythe J.R., Yost C.S.;  
 "TWIK-2, a new weak inward rectifying member of the tandem pore domain  
 potassium channel family." ;  
 RL J. Biol. Chem. 274:7887-7892(1999).  
 RN [3]  
 RP ERRATUM.  
 RA Chavez R.A., Gray A.T., Zhao B.B., Kindler C.H., Mazurek M.J.,  
 RT Mehta Y., Forsythe J.R., Yost C.S.;  
 J. Biol. Chem. 274:24440-24440(1999).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 1 AND 2), AND CHARACTERIZATION.  
 RX MEDLINE=20435832; PubMed=10887187;  
 RA Patel A.J., Maingret F., Magrone V., Fosset M., Lazdunski M.,  
 RT Honoré B.;  
 "TWIK-2, an inactivating 2P domain K<sup>+</sup> channel." ;  
 RL J. Biol. Chem. 275:28722-28730(2000).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RA Chen A.F., Gray A.T., Chen A.H., Kindler C.H., Mhatre A.N., Yost C.S.,  
 RT Lalwani A.K., Smith R.J.H.;  
 "Genomic structure and mutation screening of the TWIK-2 gene." ;  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=23388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RT Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheeler C.F., Bat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Cantino P., Prange C.,  
 RA Raha S.S., Lottelino N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McMan P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Halys S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey U., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Botterfield J.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences." ;  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC - FUNCTION: Exhibits outward rectification in a physiological K(+) gradient and mild inward rectification in symmetrical K(+) conditions.  
 CC SUBUNIT: Homodimer (Potential).  
 CC - SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC - ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1:  
 CC IsoId=Q9Y257-1; Sequence=Displayed;  
 CC Name=2:  
 CC IsoId=Q9Y257-2; Sequence=VSP 006692;  
 CC - TISSUE SPECIFICITY: WIDESPREAD EXPRESSION, DETECTED IN ALL TISSUES TESTED EXCEPT FOR SKELETAL MUSCLE. STRONGEST EXPRESSION IN PLACENTA, PANCREAS, HEART, COLON AND SPLEEN. LOWER LEVELS DETECTED IN PERIPHERAL BLOOD LEUCOCYTES, LUNG, LIVER, KIDNEY AND THYMUS.  
 CC LOWEST EXPRESSION DETECTED IN BRAIN.  
 CC - MISCELLANEOUS: INHIBITED BY INTERVAL ACIDIFICATION AND, TO A SMALL DEGREE, BY ZINC. NOT INHIBITED BY QUININE, QUINIDONE OR BARBITUM.  
 CC - SIMILARITY: Belongs to the two pore domain potassium channel family.

CC -----  
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 CC -----  
 DR EMBL; AF134149; AAD22380.1; -;  
 DR EMBL; AF117708; AAD24000.1; -;  
 DR EMBL; AF281302; AAD10506.1; -;  
 DR EMBL; AF281303; AAG10507.1; -;  
 DR EMBL; AJ297404; CAC15489.1; -;  
 DR EMBL; AJ297405; CAC15489.1; JOINED.  
 DR EMBL; BC004367; AAH04367.1; -;  
 DR Genem; HGNC:6281; KCNK6.  
 DR MIM; 603939; -;  
 DR GO; GO:0008076; C-voltage-gated potassium channel complex; TAS.  
 DR GO; GO:0005242; F-inward rectifier potassium channel activity; TAS.  
 DR GO; GO:0006813; P-potassium ion transport; TAS.  
 DR InterPro; IPR003280; K+channel\_2pore.  
 DR InterPro; IPR001622; K+channel\_pore.  
 DR InterPro; IPR001779; TWIK1\_channel.  
 DR InterPro; IPR005409; TWIK2\_channel.  
 DR InterPro; IPR005408; TWIK\_channel.  
 DR PRINTS; PR01333; 2POREKCHANEL.  
 DR PRINTS; PR01096; TWIK1CHANNEL.  
 DR PRINTS; PR01587; TWIK2CHANNEL.  
 DR PRINTS; PR01586; TWIKCHANNEL.  
 KW Transport; Ion transport; Ionic channel; Voltage-gated channel;  
 KW Potassium channel; Potassium; Transmembrane; Glycoprotein;  
 KW Alternative splicing.  
 FT DOMAIN 1 4  
 FT TRANSLEM 5 25  
 FT DOMAIN 90 115  
 FT TRANSLEM 121 141  
 FT DOMAIN 142 172  
 FT TRANSLEM 173 193  
 FT DOMAIN 199 223  
 FT TRANSLEM 236 256  
 FT DOMAIN 257 313  
 FT CARBOHYD 79 85  
 FT CARBOHYD 85 85  
 FT VARSPIC 1 134  
 FT FT  
 FT MTMGEN 53 53  
 SQ SEQUENCE 313 AA; 33747 MW; 1379382DF80575DE CRC64;  
 Query Match 16.6%; Score 348; DB 1; Length 313;  
 Best local Similarity 34.4%; Pred. No. 2.6e-17;  
 Matches 83; Conservative 42; Mismatches 104; Indels 12; Gaps 5;  
 QY 57 YLIGATVTKALQEPHEISQRTTIVIQKOTFISCHSCVNSTELDELQGVAAINAGIIP 116  
 DB 17 YLVGLALVARLEGPEARLRABLETLRQQLQSRSCVAPRLDAFVERVLAAGLGRVY 76  
 QY 117 LGNTSQNIS---HMDLSSFPFAGVTITIGFNGNISPTREGKIFCIYALGLIPDFG 172  
 DB 77 LANASSANASDPAWDFASALFFASTLTITVGQYTPITDAGKAFSIFALLGVPTWL 136  
 QY 173 LLAGVDQGTIFGKGIAYEDTFTKRVNSQTKRIRISITITILGCVLFA--LPAIF 230  
 DB 137 LITASQRIASLT---LTHVPLSMRWGMDERRRAACHVALLGVTATVCPVPAVIF 192  
 QY 231 KHI-EGMSALDAIFVYVITLTIGFDVYAGSDIE-YDFYKPYVWFILVGLAYFAV 288  
 DB 193 AHLEFMSFLDAFFFCFISLTIGGIDVYPGAPQGYALYKVLVTVYLFGLVAMLV 252  
 QY 289 L 289  
 DB 253 L 253



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Qy 167 IPFGFLAGVDQITFGKIAKVEDTE-IXNNVSOTKRIISTIFILGCVLPVAL 225
    ||| :|| : : : :|| :||
Db 118 IPULTVTPOSJGERLNNAVRRLLAAKCCGLRWTCVSTE---NLVYAGLIACAATLAL 173
    ||| :|| : : : :|| :||
Qy 226 PALIFKHIEGWSALDAIYFVVTLTITIGFDYVAGGSDIEYLDYKPVWF---WILVGL 282
    ||| :|| : : : :|| :||
Db 174 GAVAFSHFEGWTFEFHAYYCFITLTITIGFDVVALQSG-EALQKRLPYVAFSFLYILGL 232
    ||| :|| : : : :|| :||
Qy 283 AYPFAVLSMI-----GDW 295
    ||| :|| : : : :|| :||
Db 233 TVIGAFNLVLVLRFLVASADW 253
    ||| :|| : : : :|| :||

```

Search completed: July 15, 2004, 17:59:46  
 Job time : 15 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 15, 2004, 17:56:18 ; Search time 39 Seconds  
(without alignments)  
3325.076 Million cell updates/sec

Title: US-09-980-350-2

Sequence: 1 MAPPLDPSKSAONSKPRL.....LNGLTPHCAGEIAYENIK 411

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: SP archaea:\*  
2: SP bacteria:\*  
3: SP fungi:\*  
4: SP human:\*  
5: SP invertebrate:\*  
6: SP mammal:\*  
7: SP mhc:\*  
8: SP organelle:\*  
9: SP phage:\*  
10: SP plant:\*  
11: SP rodent:\*  
12: SP virus:\*  
13: SP vertebrate:\*  
14: SP unclassified:\*  
15: SP virus:\*  
16: SP bacterioph:\*  
17: SP archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2098	100.0	411	4 Q9NR72	Q9NR72 homo sapien
2	2082	99.2	411	6 Q8HY88	Q8HY88 bos taurus
3	2028	96.7	426	11 Q9Z0B6	Q9Z0B6 rattus norv
4	1248.5	59.5	453	11 Q8BZB0	Q8BZB0 mus musculu
5	1248.5	59.5	535	11 Q8BUW1	Q8BUW1 mus musculu
6	764.5	36.4	397	11 Q9Z414	Q9Z414 rattus norv
7	616	29.4	241	11 Q9CX88	Q9CX88 mus musculu
8	415	19.8	502	11 Q9TK62	Q9TK62 mus musculu
9	413	19.7	341	6 Q8RT72	Q8RT72 bos taurus
10	409.5	19.5	257	11 Q8OX50	Q8OX50 mus musculu
11	406.5	19.4	307	13 Q801T4	Q801T4 xenopus lae
12	400	19.1	184	4 Q8N4V5	Q8N4V5 homo sapien
13	380	18.1	336	11 Q8R454	Q8R454 cavia porce
14	378.5	18.0	336	11 Q9Z2T2	Q9Z2T2 rattus norv
15	377.5	18.0	336	11 Q9S199	Q9S199 mus musculu
16	372	17.7	331	13 Q8AVT5	Q8AVT5 xenopus lae

17	356.5	17.0	259	6 Q02821	Q02821 corytolagus
18	351.5	16.8	396	11 Q923V6	Q923V6 rattus norv
19	345	16.4	329	5 Q17185	Q17185 caenorhabdi
20	344	16.4	311	11 Q8B222	Q8B222 mus musculu
21	343	16.3	313	11 Q9ERU5	Q9ERU5 rattus norv
22	341	16.3	395	11 Q9JUD4	Q9JUD4 rattus norv
23	336	16.0	299	11 Q9QX34	Q9QX34 mus musculu
24	316.5	15.1	312	11 Q8R453	Q8R453 cavia porce
25	305	14.5	319	5 Q9NEV3	Q9NEV3 caenorhabdi
26	300	14.3	340	5 Q9V8R0	Q9V8R0 drosophila
27	299.5	14.3	343	11 Q9U014	Q9U014 mus musculu
28	296.5	14.1	398	5 Q9VFS9	Q9VFS9 drosophila
29	293.5	14.0	392	11 Q9ESM5	Q9ESM5 rattus norv
30	288	13.7	383	5 Q21094	Q21094 caenorhabdi
31	284.5	13.6	364	5 Q76790	Q76790 caenorhabdi
32	283.5	13.5	461	5 Q18120	Q18120 caenorhabdi
33	282	13.4	385	5 Q9V7T5	Q9V7T5 drosophila
34	279	13.3	393	5 Q9XU07	Q9XU07 caenorhabdi
35	277.5	13.2	426	5 Q816M6	Q816M6 alysia cal
36	267.5	12.8	372	5 Q7YX77	Q7YX77 caenorhabdi
37	265.5	12.7	522	5 Q22042	Q22042 caenorhabdi
38	262	12.5	452	5 Q93531	Q93531 caenorhabdi
39	262	12.5	498	5 Q22940	Q22940 caenorhabdi
40	261.5	12.5	314	11 Q8Q2Z6	Q8Q2Z6 cavia porce
41	261.5	12.5	395	5 Q9V362	Q9V362 drosophila
42	250	11.9	618	5 P90863	P90863 caenorhabdi
43	249.5	11.9	427	5 Q23386	Q23386 caenorhabdi
44	247	11.8	444	5 Q45891	Q45891 caenorhabdi
45	245.5	11.7	1357	5 Q817K7	Q817K7 caenorhabdi

#### ALIGNMENTS

RESULT 1  
Q9NR72 PRELIMINARY; PRT; 411 AA.  
ID Q9NR72  
AC Q9NR72  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Two-pore domain potassium channel TREK-1.  
GN TREK-1  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=20244931; PubMed=10784345;  
RA Meadows H.U., Benham C.D., Cairns W., Gloger I.S., Jennings C.,  
RA Medhurst A.D., Murdoch P., Chapman C.G.,  
RT "Cloning, localisation and functional expression of the human  
RT orthologue of the TREK-1 potassium channel.",  
RL PubMed Arch. 439:714-722(2000).  
DR EMBL: AF171068; AAF89743.1;  
DR GO: GO:0016021; C: integral to membrane; IEA.  
DR GO: GO:0005216; F: ion channel activity; IEA.  
DR GO: GO:0005267; F: potassium channel activity; IEA.  
DR GO: GO:0006813; P: potassium ion transport; IEA.  
DR InterPro: IPR003280; P: potassium ion transport; IEA.  
DR InterPro: IPR001622; K: channel pore.  
DR InterPro: IPR003976; K: channel pore.  
DR PRINTS: PR01333; 2E0REKCHANEL.  
DR PRINTS: PR01499; TREKCHANNEL.  
KM Ionic channel; Transmembrane.  
SQ SEQUENCE 411 AA; 45494 MW; FDE40CAB21B42A1C CRC64;

Query Match 100.0%; Score 2098; DB 4; Length 411;  
Best local similarity 100.0%; Pred. No. 2.4e-166;  
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MAAPDLDPKSAQNSKPRLSFTKPTVLAASVESDTTINWKKTVSTIFLVVLYLI 60
DB 1 MAAPDLDPKSAQNSKPRLSFTKPTVLAASVESDTTINWKKTVSTIFLVVLYLI 60
QY 61 GATVFALQEPHEISORTTIVIOKOTFISQSCVNSTELDELIOQIVAINAGIIPLCNT 120
DB 61 GATVFALQEPHEISORTTIVIOKOTFISQSCVNSTELDELIOQIVAINAGIIPLCNT 120
QY 121 SNOISHWDLGSSFFPAGVTITTTGFGNISPRTGEGKIFCIIYALLGIPFGFLLAGVDQ 180
DB 121 SNOISHWDLGSSFFPAGVTITTTGFGNISPRTGEGKIFCIIYALLGIPFGFLLAGVDQ 180
QY 181 LGTIFGKIAKVEDTIRKNNVSOTKIRIISTITIFIFGCVLFAVPAIPFKHIEGMSALD 240
DB 181 LGTIFGKIAKVEDTIRKNNVSOTKIRIISTITIFIFGCVLFAVPAIPFKHIEGMSALD 240
QY 241 AIYFVVITLTITGFGDYVAGSDIEYLDYKPVVFWIIVGLAYFAVLSMIGDMLRVIS 300
DB 241 AIYFVVITLTITGFGDYVAGSDIEYLDYKPVVFWIIVGLAYFAVLSMIGDMLRVIS 300
QY 301 KKTKEVGEFRAPAAEMTAVTAEPKETERRLSVELIDYKFORATSIKRLSALAGNHQ 360
DB 301 KKTKEVGEFRAPAAEMTAVTAEPKETERRLSVELIDYKFORATSIKRLSALAGNHQ 360
QY 361 ELTPCRRITLVNHLASERDVLPLLKTESIYINGLTPHCAGEIAVNIENIX 411
DB 361 ELTPCRRITLVNHLASERDVLPLLKTESIYINGLTPHCAGEIAVNIENIX 411

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## RESULT 2

```

Q8HY88 PRELIMINARY; PRT; 411 AA.
AC Q8HY88;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Potassium channel subfamily K member 2.
GN KCNK2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adrenal cortex;
RX PubMed=12368289;
RA Eysaert J.J., Xu L., Danthi S., Eysaert J.A.;
RT "An ACTH- and ATP-regulated Background K+ Channel in Adrenocortical
RT Cells Is TREK-1."
RL J. Biol. Chem. 277:49186-49199(2002).
DR EMBL; AY148474; AAN37591.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005677; P:potassium channel activity; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR003280; K+channel_2pore.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003976; K+channel_pore.
DR PRINTS; PRO1333; 2PORKCHANEL.
DR PRINTS; PRO1499; TREKCHANEL.
SQ SEQUENCE 411 AA; 45438 MW; A185EAC20A68CCDC CRC64;

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Query Match 99.2%; Score 2082; DB 6; Length 411;
Best Local Similarity 99.3%; Pred. No. 5.2e-165;
Matches 408; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 1 MAAPDLDPKSAQNSKPRLSFTKPTVLAASVESDTTINWKKTVSTIFLVVLYLI 60
DB 1 MAAPDLDPKSAQNSKPRLSFTKPTVLAASVESDTTINWKKTVSTIFLVVLYLI 60
QY 61 GATVFALQEPHEISORTTIVIOKOTFISQSCVNSTELDELIOQIVAINAGIIPLCNT 120
DB 61 GATVFALQEPHEISORTTIVIOKOTFISQSCVNSTELDELIOQIVAINAGIIPLCNT 120

```

```

QY 121 SNOISHWDLGSSFFPAGVTITTTGFGNISPRTGEGKIFCIIYALLGIPFGFLLAGVDQ 180
DB 121 SNOISHWDLGSSFFPAGVTITTTGFGNISPRTGEGKIFCIIYALLGIPFGFLLAGVDQ 180
QY 181 LGTIFGKIAKVEDTIRKNNVSOTKIRIISTITIFIFGCVLFAVPAIPFKHIEGMSALD 240
DB 181 LGTIFGKIAKVEDTIRKNNVSOTKIRIISTITIFIFGCVLFAVPAIPFKHIEGMSALD 240
QY 241 AIYFVVITLTITGFGDYVAGSDIEYLDYKPVVFWIIVGLAYFAVLSMIGDMLRVIS 300
DB 241 AIYFVVITLTITGFGDYVAGSDIEYLDYKPVVFWIIVGLAYFAVLSMIGDMLRVIS 300
QY 301 KKTKEVGEFRAPAAEMTAVTAEPKETERRLSVELIDYKFORATSIKRLSALAGNHQ 360
DB 301 KKTKEVGEFRAPAAEMTAVTAEPKETERRLSVELIDYKFORATSIKRLSALAGNHQ 360
QY 361 ELTPCRRITLVNHLASERDVLPLLKTESIYINGLTPHCAGEIAVNIENIX 411
DB 361 ELTPCRRITLVNHLASERDVLPLLKTESIYINGLTPHCAGEIAVNIENIX 411

```

## RESULT 3

```

Q920B6 PRELIMINARY; PRT; 426 AA.
AC Q920B6;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE 2P domain potassium channel KCNK2 (Tandem pore domain potassium
DE channel TREK-1).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=211219399; PubMed=11319556;
RA Bockenhauer D., Zilberberg N., Goldstein S.A.;
RT "KCNK2: reversible conversion of a hippocampal potassium leak into a
RT voltage-dependent channel."
RL Nat. Neurosci. 4:486-491(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar;
RX MEDLINE=21896087; PubMed=11897838;
RA Gu W., Schlichter G., Hirsch J.R., Engels H., Karschin C.,
RA Karschin A., Derst C., Steinlein O.K., Daut J.;
RT "Expression pattern and functional characteristics of two novel splice
RT variants of the two-pore-domain potassium channel TREK-2."
RL J. Physiol. 539:657-668(2002).
DR EMBL; AF325671; AAL01159.1; -.
DR EMBL; AF325671; AAL01159.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0005677; P:potassium channel activity; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR003280; K+channel_2pore.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003976; K+channel_pore.
DR PRINTS; PRO1333; 2PORKCHANEL.
DR PRINTS; PRO1499; TREKCHANEL.
KM Ionic channel; Transmembrane.
SQ SEQUENCE 426 AA; 46912 MW; CACDA05BBB95FDBC CRC64;

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Query Match 96.7%; Score 2028; DB 11; Length 426;
Best Local Similarity 95.6%; Pred. No. 1.7e-160;
Matches 393; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

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QY 1 MAAPDLDPKSAQNSKPRLSFTKPTVLAASVESDTTINWKKTVSTIFLVVLYLI 60
DB 16 VAAAPDLDPKSAQNSKPRLSFTKPTVLAASVESDTTINWKKTVSTIFLVVLYLI 75

```



QY 61 GATVFKALBOPHEISORTTIVIOKOTFISQHSQVNSTEDELIOQIVAINAGITPLGNT 120  
DB 76 GATVFKALBOPHEISORTTIVIOKONFIAQHCANSTELDELIOQIVAINAGITPLGNT 135  
QY 121 SNOISHMDLGSSEFFAGTIVITTTIGFNGISPRTEGKIFCIIYALGIPLEFGILAGVGDQ 180  
DB 136 SNOVSHMDLGSSEFFAGTIVITTTIGFNGISPRTEGKIFCIIYALGIPLEFGILAGVGDQ 195  
QY 181 LGTIFGKGIKAKVEDTIFKNNVSQTKIRIISTITFIIFGCVLPAVALPAIIFKAIIEGMSALD 240  
DB 196 LGTIFGKGIKAKVEDTIFKNNVSQTKIRIISTITFIIFGCVLPAVALPAIIFKAIIEGMSALD 255  
QY 241 AIYFVYITLTITIGFGDYVAGGSDIEYLDYKPYKVMFWMLVGLAYFAAVLSMTGDMLRVYS 300  
DB 256 AIYFVYITLTITIGFGDYVAGGSDIEYLDYKPYKVMFWMLVGLAYFAAVLSMTGDMLRVYS 315  
QY 301 KKTKEEVEGFRAHAAEWNTAVTAEFKETRRLSVEIYDKFQATSIKKXLSAELAGNNQ 360  
DB 316 KKTKEEVEGFRAHAAEWNTAVTAEFKETRRLSVEIYDKFQATSIKKXLSAELAGNNQ 375  
QY 361 ELTPCGRITLNVNHLISERDVLPPLKTESIYNGLTPHCAAGEIATVENIK 411  
DB 376 ELTPCGRITLNVNHLISERDVLPPLKTESIYNGLTPHCAAGEIATVENIK 426

## RESULT 4

QY 08BZB0 PRELIMINARY; PRT; 453 AA.  
DB 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, last sequence update)  
DE Potassium channel subfamily K member 10 (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium.  
RT "Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs."  
RL Nature 420:563-573 (2002).  
DR EMBL; AK036066; BAC29295.1; -.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005267; F:potassium channel activity; IEA.  
DR GO; GO:0006813; P:potassium ion transport; IEA.  
DR InterPro; IPR003280; K+channel\_2pore.  
DR InterPro; IPR001622; K+channel\_pore.  
DR InterPro; IPR003976; Trek channel.  
DR PRINTS; PRO1333; 2PORECHANNEL.  
DR PRINTS; PRO1499; TREKCHANNEL.  
FT NON\_TER 453  
SQ SEQUENCE 453 AA; 49958 MW; F8C5C3FF41E823B0 CRC64;

## Query Match

Best Local Similarity 59.5%; Score 1248.5; DB 11; Length 453;  
Matches 244; Conservative 58; Mismatches 65; Indels 11; Gaps 5;

QY 2 AARDLDPKSA-AQNSKRLSPSTKPTVLAASRVSDT---TINWKMKTVSTIFLVVYL 56  
DB 20 AAPVQCQPSAINGHPVPLSLISSRAVVA-RMEGASGGGLQTVWKMKTVAIFVAVV 78  
QY 57 YLIIGATVFKALBOPHEISORTTIVIOKOTFISQHSQVNSTEDELIOQIVAINAGIIP 116  
DB 79 YLVVGGVFRALBOPRESSQKNTIALBKAEFLRDHICVSPQELHTLIQHALLADNAGVSP 138  
QY 117 LGNTSNOISHMDLGSSEFFAGTIVITTTIGFNGISPRTEGKIFCIIYALGIPLEFGILAG 176

DB 139 VGNSNSSHMDLGSSEFFAGTIVITTTIGFNGISPRTEGKIFCIIYALGIPLEFGILAG 198  
QY 177 VGDOLGTIFGKGIKAKVEDTIFKNNVSQTKIRIISTITFIIFGCVLPAVALPAIIFKAIIEG 236  
DB 199 IGDOLGTIFGKGIKAKVEDTIFKNNVSQTKIRIISTITFIIFGCVLPAVALPAIIFKAIIEG 258  
QY 237 SALDAIFVYITLTITIGFGDYVAGG-SDIEYLDYKPYKVMFWMLVGLAYFAAVLSMTGDM 295  
DB 259 TALSITIFVYITLTITIGFGDYVAGGAGINRYREYKPLVFWMLVGLAYFAAVLSMTGDM 318  
QY 296 LRVISKKTKEEVEGFRAHAAEWNTAVTAEFKETRRLSVEIYDKFQATSII---KXLS 351  
DB 319 LRVISKKTKEEVEGFRAHAAEWNTAVTAEFKETRRLSVEIYDKFQATSII---KXLS 378  
QY 352 AELAGNNQELTPCGRITL 369  
DB 379 LDQRAHSLDMLSPKRSV 396

## RESULT 5

QY 08BZB0 PRELIMINARY; PRT; 535 AA.  
DB 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, last sequence update)  
DE Potassium channel subfamily K member 10.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium.  
RT "Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs."  
RL Nature 420:563-573 (2002).  
DR EMBL; AK0382153; BAC38424.1; -.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005267; F:potassium channel activity; IEA.  
DR GO; GO:0006813; P:potassium ion transport; IEA.  
DR InterPro; IPR003280; K+channel\_2pore.  
DR InterPro; IPR001622; K+channel\_pore.  
DR InterPro; IPR003976; Trek channel.  
DR PRINTS; PRO1333; 2PORECHANNEL.  
DR PRINTS; PRO1499; TREKCHANNEL.  
SQ SEQUENCE 535 AA; 59401 MW; 3598E89F875C26BD CRC64;

## Query Match

Best Local Similarity 59.5%; Score 1248.5; DB 11; Length 535;  
Matches 244; Conservative 58; Mismatches 65; Indels 11; Gaps 5;

QY 2 AARDLDPKSA-AQNSKRLSPSTKPTVLAASRVSDT---TINWKMKTVSTIFLVVYL 56  
DB 20 AAPVQCQPSAINGHPVPLSLISSRAVVA-RMEGASGGGLQTVWKMKTVAIFVAVV 78  
QY 57 YLIIGATVFKALBOPHEISORTTIVIOKOTFISQHSQVNSTEDELIOQIVAINAGIIP 116  
DB 79 YLVVGGVFRALBOPRESSQKNTIALBKAEFLRDHICVSPQELHTLIQHALLADNAGVSP 138  
QY 117 LGNTSNOISHMDLGSSEFFAGTIVITTTIGFNGISPRTEGKIFCIIYALGIPLEFGILAG 176  
DB 139 VGNSNSSHMDLGSSEFFAGTIVITTTIGFNGISPRTEGKIFCIIYALGIPLEFGILAG 198  
QY 177 VGDOLGTIFGKGIKAKVEDTIFKNNVSQTKIRIISTITFIIFGCVLPAVALPAIIFKAIIEG 236  
DB 199 IGDOLGTIFGKGIKAKVEDTIFKNNVSQTKIRIISTITFIIFGCVLPAVALPAIIFKAIIEG 258  
QY 237 SALDAIFVYITLTITIGFGDYVAGG-SDIEYLDYKPYKVMFWMLVGLAYFAAVLSMTGDM 295

Db 259 TALESIYFVVVLTITVPGDFVAGNAGINREWKPLVFWILVGLAVFAVLSMIGDW 316  
 QY 296 LRVISKKTKEEVEGFPAHAHAENTANTVAFKTERRLSYELDKQKQST---KRLKS 351  
 Db 319 LRVISKKTKEEVEGEIAPHAHAEWKAVNTAFRETRRLSYELHDKQKQKRAATIRSMERRLG 378  
 QY 352 AELAGHNOELTFRCRRL 369  
 Db 379 LDORAHSLDMLSPKRSV 396

RESULT 6  
 Q92414 PRELIMINARY; PRT; 397 AA.

AC Q92414  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Mechanosensitive tandem pore potassium channel.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RC MEDLINE=21268449; PubMed=11374070;  
 RA Kim Y., Bang H., Ghatence C., Kim D.;  
 RT "Synergistic interaction and the role of C-terminus in the activation  
 RT of PMAK K+ channels by pressure, free fatty acids and alkali";  
 RL Pflügers Arch. 442:64-72(2001).  
 DR EMBL: AF302842; AAK60504.2; -;  
 DR GO: GO:0016020; C:membrane; IEA.  
 DR GO: GO:0005216; F:ion channel activity; IEA.  
 DR GO: GO:0005267; F:potassium channel activity; IEA.  
 DR GO: GO:0006813; F:potassium ion transport; IEA.  
 DR InterPro: IPR001980; Granin.  
 DR InterPro: IPR003280; K+channel\_2pore.  
 DR InterPro: IPR001622; K+channel\_pore.  
 DR InterPro: IPR008074; TRAK channel.  
 DR Pfam: PF01271; Granin; 1.  
 DR PRINTS: PRO333; 2PORECHANNEL.  
 DR PRINTS: PRO391; TRAKCHANNEL.  
 KM Ionic channel  
 SQ SEQUENCE 397 AA; 42987 MW; 3AF04C3FPA982D22 CRC64;

Query Match 36.4%; Score 764.5; DB 11; Length 397;  
 Best Local Similarity 48.8%; Pred. No. 2.9e-55;  
 Matches 139; Conservative 57; Mismatches 86; Indels 3; Gaps 1;

QY 42 MKKKVSTIFLVVLYLIGATVFKALBPHEISORTTIVIOKQFISQHSVNSTELDE 101  
 Db 1 MRSSTLALALVLLVLSGALVFPALBPHEQVQKQKIDEDGDFLKDHPVSOKNLEG 60  
 QY 102 LIIQIVAAINAGIIP---LGNISNOISHWDGSSFFPAGTVTTTIGFNGISPRTEGGKIF 158  
 Db 61 FKLIVAEALGGGANPETSMTNSNSNLSAANLGSAPFSGTITTTIGYNIALHTDAGRLF 120  
 QY 159 CIYVALLGIPPLGFLIAGVGDQIGTIFGKIAKAVDTIKKVNOSTKRIIISTIIIFILFG 218  
 Db 121 CIFYAVVGIPLFGMLLAGVGRDGLSSLRGIGHIAVPLKMHVPDGLVPMASAVLFLILG 180  
 QY 219 CVLFEVALPAIFKEHIEGMSALDAIFYVVVTTTIGFGDVVAGSGSIEVLDKPKPVWVMI 278  
 Db 181 CILFVITLTFVFSYKMSKSKAIYFVITLTTVFGSDVPEDDGQNSPAYQPLVWVMI 240  
 QY 279 LVGLAVFAVLSMIGDWLRVISKKTKEEVEGFPAHAHAENTANTVA 323  
 Db 241 LFGLAFFASVFTTIGNMLRAVSRRTAEWGGTLTAQASMTGTIVA 285

RESULT 7  
 Q9CX88

ID Q9CX88 PRELIMINARY; PRT; 241 AA.

AC Q9CX88  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE 3010005K24Rik protein.  
 GN 3010005K24Rik.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TRISUB=Embryo;  
 RC MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Atakawa T., Hara A., Fukunishi Y., Komoto H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,  
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Glessi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schirral L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Botfield D., Bolunga N., Carninci P., de Bonaldo K.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita K., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamaya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Maeshima T., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection";  
 RL Nature 409:685-690(2001).  
 DR EMBL: AK019376; BAB31686.1; -;  
 DR MGD: MGI:1924704; 3010005K24Rik.  
 DR GO: GO:0016020; C:membrane; IEA.  
 DR GO: GO:0005267; F:potassium channel activity; IEA.  
 DR GO: GO:0006813; F:potassium ion transport; IEA.  
 DR InterPro: IPR001622; K+channel\_pore.  
 DR InterPro: IPR003976; Trek channel.  
 DR PRINTS: PRO1499; TREKCHANNEL.  
 SQ SEQUENCE 241 AA; 25799 MW; B4C39F77CD0A39DA CRC64;

Query Match 29.4%; Score 616; DB 11; Length 241;  
 Best Local Similarity 61.5%; Pred. No. 3.6e-43;  
 Matches 123; Conservative 28; Mismatches 43; Indels 6; Gaps 3;

QY 2 AAPDLDPKSA--AONSKRPLSPSTKPTVLAASVSDT---TINWKKKTVSTIFVVVL 56  
 Db 23 AAPVCGPKSATNGHHVPRRLSSRAIVYA-RMEASGGGQITWKKKTVVAFVVVV 81  
 QY 57 YLIIGATVFKALBPHEISORTTIVIOKQFISQHSVNSTELDELIQIVAAINAGIIP 116  
 Db 82 YLVTGGLVFPALBPHESSQKNTIALEKAEFRDHCIVAPQELFLIQALADNAGVSP 141  
 QY 117 LGNTSNOISHWDGSSFFPAGTVTTTIGFNGISPRTEGGKICIIYALIGPLGFLIAG 176  
 Db 142 VGNSSNSSSSWDGSAFFPAGTVTTTIGYNTAPSTGGKICILYALIGPLGFLIAG 201  
 QY 177 VGDQIGTIFGKIAKAVDTIF 196  
 Db 202 IGDQIGTIFGKIAKAVDTIF 221

RESULT 8  
 ID Q9UK62 PRELIMINARY; PRT; 502 AA.

AC Q9UK62  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

ID	Q8H2T2	PRELIMINARY;	PRT;	341 AA.
AC	Q8H2T2			
DT	01-MAR-2003 (TREMBlrel, 23, Created)			
DT	01-MAR-2003 (TREMBlrel, 23, Last sequence update)			
DT	01-JUN-2003 (TREMBlrel, 24, Last annotation update)			
DE	Potassium channel TASK-4.			
GN	KCNK17.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Despot C., Rengnanta V.K., Preisig-Mueller R., Rajan S., Daut U.;			
RT	"Cloning and sequencing of bovine potassium channel TASK-4.";			
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF479760; AAN32894.1; -			
DR	GO; GO:0016020; C:membrane; IEA.			
DR	GO; GO:0005267; F:potassium channel activity; IEA.			
DR	GO; GO:0006813; P:potassium ion transport; IEA.			
DR	InterPro; IPR003280; K+channel_2pore.			
DR	InterPro; IPR001622; K+channel_pore.			
DR	InterPro; IPR003092; TASK_Channel.			
DR	PRINTS; PR01333; 2PORECHANNEL.			
DR	PRINTS; PR01095; TASKCHANNEL.			
SO	SEQUENCE 341 AA; 37695 MW; 0A21FEEA71B39401 CRC64;			
Query Match	19.7%; Score 413; DB 6; Length 341;			
Best Local Similarity	37.2%; Pred. No. 4.5e-26;			
Matches 93; Conservative 53; Mismatches 92; Indels 12; Gaps 6;				
QY	48 STIFLVV--LVLYIGATVFKALQGP--HEHSORTTIVIQKQFISQHSCTNRELMELI 103			
DB	35 STILLILTYITVYLVGICVFWALESPAHDSKR--FQDKMALIRNFTLIDGANDSLI 92			
QY	104 QQIVAAINAGIIPLGNTSNQISHWDSGSEFFAGTVITTTGNGNISPRTEGKIFCIYA 163			
DB	93 RGIIEAYKNDIVLGNTTS-MGRMEFVGSFFSVSTITTTGCGNLSRPTMAARLFCIFPA 151			
QY	164 LIGIPLEGFLLAGVDDGLITFGGIKAVEDTFLKMWVSQTKRILITITIFILFGCVLFV 223			
DB	152 LVGIPLVLVVL---NRLGHCMQGVHRCARRLGGAKWDPAKAWMLAGSSALISGLLFL 207			
QY	224 ALPAIIFKHIEGMSALDAIFVYVITTTITFGDVPVAG--GSDIEVLDYKQPVVFWIIVGL 282			
DB	208 LLPELPLFNHHEGWTYVGVFFSFYTLSTVGFGDVIIGMNSRNPPLYMYQNTVSLMILFGM 267			
QY	283 AYPAVALISM 292			
DB	268 AWTALLIKLI 277			
RESULT 10				
Q8HXEO				
ID	Q8HXEO	PRELIMINARY;	PRT;	257 AA.
AC	Q8HXEO			
DT	01-JUN-2003 (TREMBlrel, 24, Created)			
DT	01-JUN-2003 (TREMBlrel, 24, Last sequence update)			
DT	01-OCT-2003 (TREMBlrel, 25, Last annotation update)			
DE	Mus musculus (Mouse).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	STRAIN=FVB/N; TISSUE=Colon;			
RL	Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC051088; AAH51088.1; -			
DR	GO; GO:0016020; C:membrane; IEA.			





Query Match	18.0%;	Score 377.5;	DB 11;	Length 336;
Best Local Similarity	34.3%;	Pred. No. 4e-23;		
Matches 84;	Conservative 57;	Mismatches 93;	Indels 11;	Gaps 7;

QY 5 FLVV--VLKLVIGATVFLKALBEGHEHISORTIVVOKQTFISQSCVNSNTELDLQIYA 108  
 Db 25 FLVLGLVLVLVGAIVAVFSSVFLPYDDLROSLRKLRFLFEHHCISEPDLDFLORVIE 84  
 QY 109 AINAGIIPLGNTSNOISHMDLGSEFFPAGTVITTTIGFNISPRTEGGKICITVALLGP 168  
 Db 85 ASNVGYSVLSNAGN--WMDFTSALFFASIVLSTTGGHTVPLSDGKAFCTIVSICIP 143  
 QY 169 LSEFLAGVGDOGLTIFCGKIAKVEDPFIKXNSQTKIRISLTII--FLIGCVFVAPL 226  
 Db 144 FTLLFETANVQRYVYHVR--RPVLYFIRIRGSEKQVVALVHVLGFTVSCFEFT--P 199  
 QY 227 AIIFKHIE--GMSALDAIVFVITLTITGEGDYAG--GSDIEYLDFFKPVVWEMILVGLAY 284  
 Db 200 AAFVSFLVEDMNNFLSEFFCFISLSTIGLGYVGEQYNQKRELKYGITCYLLGLIA 259  
 QY 285 FAVVL 289  
 Db 260 MLVVL 264

Search completed: July 15, 2004, 18:00:37  
Job time : 41 secs



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Db 121 SNOISHWDLGSSFFFACTVITTTIGFNGISPRTEGKIFCIIYALLGLPLFGFLAGVGDQ 180
Qy 181 LGTFEGGIKAVEDTFTKXNVSOQTKRIISTITIFILFGCVLPVALPAITFKHIEGMSALD 240
Db 181 LGTFEGGIKAVEDTFTKXNVSOQTKRIISTITIFILFGCVLPVALPAITFKHIEGMSALD 240
Qy 241 AITFVVITLTTTIGFGDYVAGSDIEYDFFKPVVFWMIIVGLAYFAAVLSMIGDWLRVIS 300
Db 241 AITFVVITLTTTIGFGDYVAGSDIEYDFFKPVVFWMIIVGLAYFAAVLSMIGDWLRVIS 300
Qy 301 KKTKEEVEGFRPAAAEWTANTVTAIEFKETRRRLSVEIYDKFORATSIRKLSAELAGNHNQ 360
Db 301 KKTKEEVEGFRPAAAEWTANTVTAIEFKETRRRLSVEIYDKFORATSIRKLSAELAGNHNQ 360
Qy 361 ELTPCRRRLSVNHLTSEBDVLPPLTKTESIYLNGLPHCGAGEIAVIENTIK 411
Db 361 ELTPCRRRLSVNHLTSEBDVLPPLTKTESIYLNGLPHCGAGEIAVIENTIK 411

```

# RESULT 2

```

US-10-121-746-83
; Sequence 83, Application US/10121746
; Publication No. US20030036648A1
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. US20030036648A1e1 Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/10/121,746
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US/09/336,643A
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 411
; TYPE: PRT
; ORGANISM: H. sapiens
US-10-121-746-83

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Query Match 100.0%; Score 2098; DB 14; Length 411;  
 Best Local Similarity 100.0%; Pred. No. 2,4e-197; Indels 0; Gaps 0;  
 Matches 411; Conservative 0; Mismatches 0;

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Qy 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTGSTIFLVVLYLI 60
Db 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTGSTIFLVVLYLI 60
Qy 61 GATVFKALBOPHEISORTTIVIOKOTFISQSCVNSTEDELIOQIVAAINAGIPLGNT 120
Db 61 GATVFKALBOPHEISORTTIVIOKOTFISQSCVNSTEDELIOQIVAAINAGIPLGNT 120
Qy 121 SNOISHWDLGSSFFFACTVITTTIGFNGISPRTEGKIFCIIYALLGLPLFGFLAGVGDQ 180
Db 121 SNOISHWDLGSSFFFACTVITTTIGFNGISPRTEGKIFCIIYALLGLPLFGFLAGVGDQ 180
Qy 181 LGTFEGGIKAVEDTFTKXNVSOQTKRIISTITIFILFGCVLPVALPAITFKHIEGMSALD 240
Db 181 LGTFEGGIKAVEDTFTKXNVSOQTKRIISTITIFILFGCVLPVALPAITFKHIEGMSALD 240
Qy 241 AITFVVITLTTTIGFGDYVAGSDIEYDFFKPVVFWMIIVGLAYFAAVLSMIGDWLRVIS 300
Db 241 AITFVVITLTTTIGFGDYVAGSDIEYDFFKPVVFWMIIVGLAYFAAVLSMIGDWLRVIS 300

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Qy 301 KKTKEEVEGFRPAAAEWTANTVTAIEFKETRRRLSVEIYDKFORATSIRKLSAELAGNHNQ 360
Db 301 KKTKEEVEGFRPAAAEWTANTVTAIEFKETRRRLSVEIYDKFORATSIRKLSAELAGNHNQ 360
Qy 361 ELTPCRRRLSVNHLTSEBDVLPPLTKTESIYLNGLPHCGAGEIAVIENTIK 411
Db 361 ELTPCRRRLSVNHLTSEBDVLPPLTKTESIYLNGLPHCGAGEIAVIENTIK 411

```

# RESULT 3

```

US-09-892-360-18
; Sequence 18, Application US/09892360
; Publication No. US20040101833A1
; GENERAL INFORMATION:
; APPLICANT: LAZDUNSKI, MICHEL
; APPLICANT: LESAGE, FLORIAN
; APPLICANT: ROMERY, GEORGES
; TITLE OF INVENTION: HUMAN TRK2, A STRETCH-AND ARACHIDONIC ACID-SENSITIVE
; TITLE OF INVENTION: K+ CHANNEL ACTIVATED BY INHALANTIONAL ANESTHETICS AND
; FILE REFERENCE: 1256-R-00
; CURRENT APPLICATION NUMBER: US/09/892,360
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 60/214,559
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 18
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-892-360-18

```

Query Match 99.8%; Score 2095; DB 12; Length 411;  
 Best Local Similarity 99.8%; Pred. No. 4,8e-197;  
 Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTGSTIFLVVLYLI 60
Db 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTGSTIFLVVLYLI 60
Qy 61 GATVFKALBOPHEISORTTIVIOKOTFISQSCVNSTEDELIOQIVAAINAGIPLGNT 120
Db 61 GATVFKALBOPHEISORTTIVIOKOTFISQSCVNSTEDELIOQIVAAINAGIPLGNT 120
Qy 121 SNOISHWDLGSSFFFACTVITTTIGFNGISPRTEGKIFCIIYALLGLPLFGFLAGVGDQ 180
Db 121 SNOISHWDLGSSFFFACTVITTTIGFNGISPRTEGKIFCIIYALLGLPLFGFLAGVGDQ 180
Qy 181 LGTFEGGIKAVEDTFTKXNVSOQTKRIISTITIFILFGCVLPVALPAITFKHIEGMSALD 240
Db 181 LGTFEGGIKAVEDTFTKXNVSOQTKRIISTITIFILFGCVLPVALPAITFKHIEGMSALD 240
Qy 241 AITFVVITLTTTIGFGDYVAGSDIEYDFFKPVVFWMIIVGLAYFAAVLSMIGDWLRVIS 300
Db 241 AITFVVITLTTTIGFGDYVAGSDIEYDFFKPVVFWMIIVGLAYFAAVLSMIGDWLRVIS 300
Qy 301 KKTKEEVEGFRPAAAEWTANTVTAIEFKETRRRLSVEIYDKFORATSIRKLSAELAGNHNQ 360
Db 301 KKTKEEVEGFRPAAAEWTANTVTAIEFKETRRRLSVEIYDKFORATSIRKLSAELAGNHNQ 360
Qy 361 ELTPCRRRLSVNHLTSEBDVLPPLTKTESIYLNGLPHCGAGEIAVIENTIK 411
Db 361 ELTPCRRRLSVNHLTSEBDVLPPLTKTESIYLNGLPHCGAGEIAVIENTIK 411

```

# RESULT 4

```

US-08-816-011-45
; Sequence 45, Application US/08816011
; Publication No. US20030165806A1
; GENERAL INFORMATION:
; APPLICANT: Price, Laura A.

```



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; APPLICANT: Pausch, Mark H.
; TITLE OF INVENTION: Potassium Channels, Nucleotide Sequences
; TITLE OF INVENTION: Encoding Them, and Methods of Using Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Home Products Corporation
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,011
; FILING DATE: 11-MAR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthews, Gale F.
; REGISTRATION NUMBER: 32,269
; REFERENCE/DOCKET NUMBER: 32,421-C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-683-2134
; TELEFAX: 201-683-4117
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-816-011-45

```

```

Query Match          98.4%; Score 2065; DB 8; Length 426;
Best Local Similarity 98.8%; Pred. No. 4,5e-194;
Matches 406; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

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QY 1 MAAPDLDPKSAONSKRSLFSKPTVLASRVESDTTINVMKKTSTIFLVVLYLI 60
DB 16 VAAEDLDLPKSAONSKRSLFSKPTVLASRVESDTTINVMKKTSTIFLVVLYLI 75
QY 61 GATVFKALEOPHEISQRTTIVIOKQTFISQHSQVNSTELDELIOQIVAAINAGIIPLGNT 120
DB 76 GATVFKALEOPHEISQRTTIVIOKQTFISQHSQVNSTELDELIOQIVAAINAGIIPLGNT 135
QY 121 SNOISHWDLGSSFFPAGVTITIGFNGISPRTEGGKICIIYALGIPFGLLAGVGDQ 180
DB 136 SNOISHWDLGSSFFPAGVTITIGFNGISPRTEGGKICIIYALGIPFGLLAGVGDQ 195
QY 181 LGTFGKGIAKVEDTFIKMNSQTKIRIISTIFILFGCVLPAALPAIFKHIEGMSALD 240
DB 196 LGTFGKGIAKVEDTFIKMNSQTKIRIISTIFILFGCVLPAALPAIFKHIEGMSALD 255
QY 241 AIYFVVTITLTIGFGDYVAGSDIEYDFFKPVVWFILVGLAFAAVALSMIGWLRLVIS 300
DB 256 AIYFVVTITLTIGFGDYVAGSDIEYDFFKPVVWFILVGLAFAAVALSMIGWLRLVIS 315
QY 301 KKTKEEVEGFRAHAEMTANTATAFKETRRLSVEIYDKFORATSIKRLSABELAGNHQ 360
DB 316 KKTKEEVEGFRAHAEMTANTATAFKETRRLSVEIYDKFORATSIKRLSABELAGNHQ 375
QY 361 ELTPCRRRLTSVNHLTSEEDVLPPLKTESIYINGLTPHACGEIAVNIENIK 411
DB 376 ELTPCRRRLTSVNHLTSEEDVLPPLKTESIYINGLTPHACGEIAVNIENIK 426

```

```

RESULT 5
US-09-828-746-6
; Sequence 6, Application US/09828746
; Patent No. US20020028485A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Helen Jane Meadows
; APPLICANT: Conrad Gerald Chapman
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30031-D1
; CURRENT APPLICATION NUMBER: US/09/828,746
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 09/236,080
; PRIOR FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: EP 98300570.3
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: UK 9822135.1
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 411
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
;
US-09-828-746-6

```

```

Query Match          97.1%; Score 2038; DB 9; Length 411;
Best Local Similarity 96.1%; Pred. No. 1,9e-191;
Matches 395; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

```

```

QY 1 MAAPDLDPKSAONSKRSLFSKPTVLASRVESDTTINVMKKTSTIFLVVLYLI 60
DB 1 MAAPDLDPKSAONSKRSLFSKPTVLASRVESDTTINVMKKTSTIFLVVLYLI 60
QY 61 GATVFKALEOPHEISQRTTIVIOKQTFISQHSQVNSTELDELIOQIVAAINAGIIPLGNT 120
DB 61 GATVFKALEOPHEISQRTTIVIOKQTFISQHSQVNSTELDELIOQIVAAINAGIIPLGNT 120
QY 121 SNOISHWDLGSSFFPAGVTITIGFNGISPRTEGGKICIIYALGIPFGLLAGVGDQ 180
DB 121 SNOISHWDLGSSFFPAGVTITIGFNGISPRTEGGKICIIYALGIPFGLLAGVGDQ 180
QY 181 LGTFGKGIAKVEDTFIKMNSQTKIRIISTIFILFGCVLPAALPAIFKHIEGMSALD 240
DB 181 LGTFGKGIAKVEDTFIKMNSQTKIRIISTIFILFGCVLPAALPAIFKHIEGMSALD 240
QY 241 AIYFVVTITLTIGFGDYVAGSDIEYDFFKPVVWFILVGLAFAAVALSMIGWLRLVIS 300
DB 241 AIYFVVTITLTIGFGDYVAGSDIEYDFFKPVVWFILVGLAFAAVALSMIGWLRLVIS 300
QY 301 KKTKEEVEGFRAHAEMTANTATAFKETRRLSVEIYDKFORATSIKRLSABELAGNHQ 360
DB 301 KKTKEEVEGFRAHAEMTANTATAFKETRRLSVEIYDKFORATSIKRLSABELAGNHQ 360
QY 361 ELTPCRRRLTSVNHLTSEEDVLPPLKTESIYINGLTPHACGEIAVNIENIK 411
DB 361 ELTPCRRRLTSVNHLTSEEDVLPPLKTESIYINGLTPHACGEIAVNIENIK 411

```

```

RESULT 6
US-09-939-484-8
; Sequence 8, Application US/09939484
; Patent No. US20020032322A1
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Lazard, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; FILE REFERENCE: 1201-CIP-01V-00
; CURRENT APPLICATION NUMBER: US/09/939,484
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/144,914
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 08/749,816
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: 60/095,234
; PRIOR FILING DATE: 1998-08-04

```

; PRIOR APPLICATION NUMBER: FR 96/01565  
 ; PRIOR FILING DATE: 1996-02-08  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: Patent Ver. 2.0  
 ; SEQ ID NO 8  
 ; LENGTH: 370  
 ; TYPE: PRT  
 ; ORGANISM: Murine  
 ; FEATURE:  
 ; OTHER INFORMATION: TREK-1  
 US-09-939-484-8

Query Match 86.9%; Score 1824; DB 9; Length 370;  
 Best Local Similarity 96.5%; Pred. No. 1,8e-170;  
 Matches 355; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDPTINVMKKTSTIFLVVLYLI 60  
 DB 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDPTINVMKKTSTIFLVVLYLI 60  
 QY 61 GATVFKALBOPHEISQRTTIVIOKOTFISQHSQVNSTELDELICQIVAAINAGIIPLGNT 120  
 DB 61 GATVFKALBOPHEISQRTTIVIOKOTFISQHSQVNSTELDELICQIVAAINAGIIPLGNS 120  
 QY 121 SNOISHMDLGSFFPAGTIVTTTIGFNGISPRTEGKIFCIYVALLGIPLEGFLAGVDQ 180  
 DB 121 SNOVSHMDLGSFFPAGTIVTTTIGFNGISPRTEGKIFCIYVALLGIPLEGFLAGVDQ 180  
 QY 181 LGTIFGKIAKVEDTFIKMNVSTQKRIISTIIIFILEGCVLPVALPAVIFKHEIGMSALD 240  
 DB 181 LGTIFGKIAKVEDTFIKMNVSTQKRIISTIIIFILEGCVLPVALPAVIFKHEIGMSALD 240  
 QY 241 AIFVAVITLTITIGFDYVAGSDIEYDFKPVVFWIIVGLAFVAVISMIGDMLRVIS 300  
 DB 241 AIFVAVITLTITIGFDYVAGSDIEYDFKPVVFWIIVGLAFVAVISMIGDMLRVIS 300  
 QY 301 KKTKEEVEGFRRAHAEMTAVTAEFKETRRLSVEIYDKFORATSIRKLSAELAGNHQ 360  
 DB 301 KKTKEEVEGFRRAHAEMTAVTAEFKETRRLSVEIYDKFORATSIRKLSAELAGNHQ 360  
 QY 361 ELTPCRR 368  
 DB 361 ELTPCRR 368

RESULT 7  
 US-09-939-483-8  
 ; Sequence 8, Application US/09939483  
 ; Patent No. US2002009458A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Duprat, Fabrice  
 ; APPLICANT: Lesage, Florian  
 ; APPLICANT: Fink, Michel  
 ; APPLICANT: Lazdunski, Michel  
 ; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING  
 ; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS  
 ; FILE REFERENCE: 1201-CIP-DIV-2-00  
 ; CURRENT APPLICATION NUMBER: US/09/939,483  
 ; PRIOR FILING DATE: 2001-08-24  
 ; PRIOR APPLICATION NUMBER: 09/144,914  
 ; PRIOR FILING DATE: 1998-09-01  
 ; PRIOR APPLICATION NUMBER: 08/749,816  
 ; PRIOR FILING DATE: 1996-11-15  
 ; PRIOR APPLICATION NUMBER: 60/095,234  
 ; PRIOR FILING DATE: 1998-08-04  
 ; PRIOR APPLICATION NUMBER: FR 96/01565  
 ; PRIOR FILING DATE: 1996-02-08  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: Patent Ver. 2.0  
 ; SEQ ID NO 8  
 ; LENGTH: 370  
 ; TYPE: PRT  
 ; ORGANISM: Murine

; FEATURE:  
 ; OTHER INFORMATION: TREK-1  
 US-09-939-483-8

Query Match 86.9%; Score 1824; DB 9; Length 370;  
 Best Local Similarity 96.5%; Pred. No. 1,8e-170;  
 Matches 355; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDPTINVMKKTSTIFLVVLYLI 60  
 DB 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDPTINVMKKTSTIFLVVLYLI 60  
 QY 61 GATVFKALBOPHEISQRTTIVIOKOTFISQHSQVNSTELDELICQIVAAINAGIIPLGNT 120  
 DB 61 GATVFKALBOPHEISQRTTIVIOKOTFISQHSQVNSTELDELICQIVAAINAGIIPLGNS 120  
 QY 121 SNOISHMDLGSFFPAGTIVTTTIGFNGISPRTEGKIFCIYVALLGIPLEGFLAGVDQ 180  
 DB 121 SNOVSHMDLGSFFPAGTIVTTTIGFNGISPRTEGKIFCIYVALLGIPLEGFLAGVDQ 180  
 QY 181 LGTIFGKIAKVEDTFIKMNVSTQKRIISTIIIFILEGCVLPVALPAVIFKHEIGMSALD 240  
 DB 181 LGTIFGKIAKVEDTFIKMNVSTQKRIISTIIIFILEGCVLPVALPAVIFKHEIGMSALD 240  
 QY 241 AIFVAVITLTITIGFDYVAGSDIEYDFKPVVFWIIVGLAFVAVISMIGDMLRVIS 300  
 DB 241 AIFVAVITLTITIGFDYVAGSDIEYDFKPVVFWIIVGLAFVAVISMIGDMLRVIS 300  
 QY 301 KKTKEEVEGFRRAHAEMTAVTAEFKETRRLSVEIYDKFORATSIRKLSAELAGNHQ 360  
 DB 301 KKTKEEVEGFRRAHAEMTAVTAEFKETRRLSVEIYDKFORATSIRKLSAELAGNHQ 360  
 QY 361 ELTPCRR 368  
 DB 361 ELTPCRR 368

RESULT 8  
 US-09-729-920-5  
 ; Sequence 5, Application US/09729920  
 ; Patent No. US20020103115A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GUEGLER, Karl et al  
 ; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
 ; TITLE OF INVENTION: AND USES THEREOF  
 ; FILE REFERENCE: C0000858  
 ; CURRENT APPLICATION NUMBER: US/09/729,920  
 ; PRIOR FILING DATE: 2000-12-06  
 ; NUMBER OF SEQ ID NOS: 5  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 5  
 ; LENGTH: 538  
 ; TYPE: PRT  
 ; ORGANISM: Rattus norvegicus  
 US-09-729-920-5

Query Match 59.5%; Score 1248.5; DB 9; Length 538;  
 Best Local Similarity 64.6%; Pred. No. 1,2e-113;  
 Matches 244; Conservative 58; Mismatches 65; Indels 11; Gaps 5;

QY 2 MAAPDLDPKSA--AQNPKRLSFTKPTVLASRVESDT--TINVMKKTSTIFLVVLY 56  
 DB 23 AAPPVCPKSKATNGHPVLPSTISSRATVVA--RMGASOGGQGTQVWKMTVAIFVVVVV 81  
 QY 57 YLIIGATVPKALBOPHEISQRTTIVIOKOTFISQHSQVNSTELDELICQIVAAINAGIIP 116  
 DB 82 YLVATGIVFRALBOPHEISQRTTIVIOKOTFISQHSQVNSTELDELICQIVAAINAGIIP 141  
 QY 117 LGNTSNOISHMDLGSFFPAGTIVTTTIGFNGISPRTEGKIFCIYVALLGIPLEGFLAG 176  
 DB 142 VGNSSNSHMDLGSFAFPAGTIVTTTIGYGNIAIPSTEGKIFCIYVALLGIPLEGFLAG 201



Query Match 59.2%; Score 1242.5; DB 9; Length 543;  
 Best Local Similarity 63.5%; Pred. No. 4.8e-113;  
 Matches 244; Conservative 57; Mismatches 66; Indels 17; Gaps 5;

QY 2 AADPLDPKSA-----AONSKPRISFSTKPTVLASRVESDT--TINWKKMTVSTI 50  
 DB 22 AAAPVCCPKSATNGQPAPAPAPPTPTPLRSLISSRATVVA-RMEGTSQGLQTVWKKMTVVAI 80  
 QY 51 FLVVVYLLIIGATVFKALBQPHISORTTIVIOKQTFISQHSQVNSTEIDELIQOVAI 110  
 DB 81 FVVVVVYLVGGLVFRLEQPFESSQCNITALEKAEFLDHCVCVSQBELITLQHALDD 140  
 QY 111 NAGIIPGNTSNOISHWDLSSFFPAGTVTTTIGFNGISPRTEGGKIFCIYVALLGIPLF 170  
 DB 141 NAGVSPFGNSNNSSHWDLSAFAFFAGTVTTTIGYGNIAPEEGKIFCIYVAILGIPLF 200  
 QY 171 GELLAGVDGLTTFGKIAKVEDTFTKMWVSOQTKIRIISTITFIIFGCVLVAIPAIF 230  
 DB 201 GFLLAGIGDGLTFPGKSIARVEKVRKKQVSOQTKIRIVSTILFILAQIVFVITPAVIF 260  
 QY 231 KHIEGMSALDAIFYVYVITLTITIGFGDYVAGG-SDIEYLDIFYKVVWFVILVGLAYFAVL 289  
 DB 261 KYIEGWTALBSIFVVVYVLTITVGFDPFVAGNGANGIYREMYKPLVWFVILVGLAYFAVL 320  
 QY 290 SMIGDWLRVYSKKTKEEVGEFRHAAAEWNTAETKETERRRLSVETIYKFORATSI--- 346  
 DB 321 SMIGDWLRVYSKKTKEEVGIRKAAAEWNTAETKETERRRLSVETIYKFORATSI--- 380  
 QY 347 -KRLSALAGNNOEITPCRTU 369  
 DB 381 ERRRLGIDQRAHSLDWLSPEKRSV 404

RESULT 12  
 US-10-262-511-106  
 ; Sequence 106, Application US/10262511  
 ; Publication No. US20040038223A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Smithson, Glenda  
 ; APPLICANT: Mallet, Isabelle  
 ; APPLICANT: Peyman, John A.  
 ; APPLICANT: Kekuda, Ramesh  
 ; APPLICANT: Ut, Jingfang  
 ; APPLICANT: Li, Li  
 ; APPLICANT: Guo, Xiaojie (Sasha)  
 ; APPLICANT: Patuturajan, Meera  
 ; APPLICANT: Szytek, Kimberly A.  
 ; APPLICANT: Edinger, Shlomit R.  
 ; APPLICANT: Ellerman, Karen  
 ; APPLICANT: Malvankar, Uriel M.  
 ; APPLICANT: Ort, Tatiana  
 ; APPLICANT: Gortman, Linda  
 ; APPLICANT: Zehnusen, Bryan D.  
 ; APPLICANT: Anderson, David W.  
 ; APPLICANT: Zhong, Mei  
 ; APPLICANT: Catterton, Elina  
 ; APPLICANT: Ji, Weizhen  
 ; APPLICANT: Miller, Charles E.  
 ; APPLICANT: Rastelli, Luca  
 ; APPLICANT: Stone, David J.  
 ; APPLICANT: Pena, Carol E. A.  
 ; APPLICANT: Shenoy, Suresh G.  
 ; APPLICANT: Shimkets, Richard A.  
 ; APPLICANT: Rothenberg, Mark E.  
 ; APPLICANT: Leach, Martin D.  
 ; APPLICANT: Agee, Michele L.  
 ; APPLICANT: Bergins, Constance  
 ; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
 ; FILE REFERENCE: 21402-462C  
 ; CURRENT APPLICATION NUMBER: US/10/262,511  
 ; CURRENT FILING DATE: 2003-05-28  
 ; PRIOR APPLICATION NUMBER: 60/326,483

;; PRIOR FILING DATE: 2001-10-02  
 ;; PRIOR APPLICATION NUMBER: 60/373,815  
 ;; PRIOR FILING DATE: 2002-04-19  
 ;; PRIOR APPLICATION NUMBER: 60/327,917  
 ;; PRIOR FILING DATE: 2001-10-09  
 ;; PRIOR APPLICATION NUMBER: 60/381,642  
 ;; PRIOR FILING DATE: 2002-05-17  
 ;; PRIOR APPLICATION NUMBER: 60/328,029  
 ;; PRIOR FILING DATE: 2002-10-09  
 ;; PRIOR APPLICATION NUMBER: 60/381,038  
 ;; PRIOR FILING DATE: 2002-05-16  
 ;; PRIOR APPLICATION NUMBER: 60/328,056  
 ;; PRIOR FILING DATE: 2001-10-09  
 ;; PRIOR APPLICATION NUMBER: 60/373,260  
 ;; PRIOR FILING DATE: 2002-04-17  
 ;; PRIOR APPLICATION NUMBER: 60/373,826  
 ;; PRIOR FILING DATE: 2002-04-19  
 ;; PRIOR APPLICATION NUMBER: 60/327,435  
 ;; PRIOR FILING DATE: 2001-10-05  
 ;; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ;; NUMBER OF SEQ ID NOS: 439  
 ;; SOFTWARE: Cursesqlist version 0.1  
 ;; SEQ ID NO 106  
 ;; LENGTH: 543  
 ;; TYPE: PRT  
 ;; ORGANISM: Homo sapiens  
 US-10-262-511-106

Query Match 59.2%; Score 1242.5; DB 12; Length 543;  
 Best Local Similarity 63.5%; Pred. No. 4.8e-113;  
 Matches 244; Conservative 57; Mismatches 66; Indels 17; Gaps 5;

QY 2 AADPLDPKSA-----AONSKPRISFSTKPTVLASRVESDT--TINWKKMTVSTI 50  
 DB 22 AAAPVCCPKSATNGQPAPAPAPPTPTPLRSLISSRATVVA-RMEGTSQGLQTVWKKMTVVAI 80  
 QY 51 FLVVVYLLIIGATVFKALBQPHISORTTIVIOKQTFISQHSQVNSTEIDELIQOVAI 110  
 DB 81 FVVVVVYLVGGLVFRLEQPFESSQCNITALEKAEFLDHCVCVSQBELITLQHALDD 140  
 QY 111 NAGIIPGNTSNOISHWDLSSFFPAGTVTTTIGFNGISPRTEGGKIFCIYVALLGIPLF 170  
 DB 141 NAGVSPFGNSNNSSHWDLSAFAFFAGTVTTTIGYGNIAPEEGKIFCIYVAILGIPLF 200  
 QY 171 GELLAGVDGLTTFGKIAKVEDTFTKMWVSOQTKIRIISTITFIIFGCVLVAIPAIF 230  
 DB 201 GFLLAGIGDGLTFPGKSIARVEKVRKKQVSOQTKIRIVSTILFILAQIVFVITPAVIF 260  
 QY 231 KHIEGMSALDAIFYVYVITLTITIGFGDYVAGG-SDIEYLDIFYKVVWFVILVGLAYFAVL 289  
 DB 261 KYIEGWTALBSIFVVVYVLTITVGFDPFVAGNGANGIYREMYKPLVWFVILVGLAYFAVL 320  
 QY 290 SMIGDWLRVYSKKTKEEVGEFRHAAAEWNTAETKETERRRLSVETIYKFORATSI--- 346  
 DB 321 SMIGDWLRVYSKKTKEEVGIRKAAAEWNTAETKETERRRLSVETIYKFORATSI--- 380  
 QY 347 -KRLSALAGNNOEITPCRTU 369  
 DB 381 ERRRLGIDQRAHSLDWLSPEKRSV 404

RESULT 13  
 US-09-852-386-73  
 ; Sequence 73, Application US/09852386  
 ; Publication No. US20030064433A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Roderick, Steven L.  
 ; APPLICANT: Benjamin, Christopher  
 ; APPLICANT: Karnovsky, Alla M.  
 ; APPLICANT: Ruble, Cara L.  
 ; TITLE OF INVENTION: Human Ion Channels  
 ; FILE REFERENCE: 00133 US1  
 ; CURRENT APPLICATION NUMBER: US/09/852,386

```

; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,305
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 60/207,092
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/206,526
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,033
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/207,093
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/216,893
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 60/237,873
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: 60/223,245
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 73
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-386-73

```

```

Query Match      59.2%; Score 1242.5; DB 12; Length 543;
Best Local Similarity 63.5%; Pred. No. 4,8e-113;
Matches 244; Conservative 57; Mismatches 66; Indels 17; Gaps 5;

```

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QY 2 AADPLDPKSA-----AQNPKRLSFTKPTVLAASRVSDT---TINMKKTKVSTI 50
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 22 AAAPVQPKSATNGQPPAPAPPTPTPRISISSRATVVA-RMEGTSQGGLOTVMKMTVAI 80
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 51 FLVVVLIITGATVFKALEQPHETISORTTIVIOKOTFISCHSCVNSTELDELIOQIVAAI 110
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 81 FVVVVVIVTGVFRLAEQPFESSQKNTIALERAEFLRDHVCSPOLETLIGHALDAD 140
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 111 NAGIIPLGNTSNQISHWDLGSSFFPAGTIVTTTIGFNGISPRTEGKIFCIYALGIPLF 170
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 141 NAGVSPIGNSSNSHMDLGSAFFPAGTIVTTTIGYGNIAPESTEGKIFCIYALGIPLF 200
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 171 GFLLAGVDOLGTTFGKIAKVEDTPIKMNVSQTKIRIISTITIFLPGCVFLPALPAIIF 230
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 201 GFLLAGVDOLGTTFGKISIAVEKVPKQVSQTKIRIVSTILFILAQCTVFYTIYAVIF 260
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 231 KHIEGMSALDAIYFVVVITLTTFGFDYVAGG-SDIEYLDIFYKPVWFWIIVGLAYFAAVL 289
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 261 KYIEGWTALSIYFVVVITLTTFGFDYVAGGAGINVRKYLFWFWIIVGLAYFAAVL 320
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 290 SMIGDMWRVLSKTKKEVEGFRAHAAMTANVTAPEFETRRRLSVEIYDKFORATSI--- 346
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 321 SMIGDMWRVLSKTKKEVEGEIKAHAAEMKANVTAPEFETRRRLSVEIYDKFORATSI--- 380
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 347 -KRLSAELAGNHQELTPCRTL 369
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 381 ERRRLGIDQRAHSLDMLSPKRSV 404
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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RESULT 14
US-10-332-175-2
; Sequence 2, Application US/10332175
; Publication No. US20030176342A1
; GENERAL INFORMATION:
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: No. US20030176342A1el potassium channel
; FILE REFERENCE: Y0133PCT-666
; CURRENT APPLICATION NUMBER: US/10/332,175
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: JP 2000-396020
; PRIOR FILING DATE: 2000-12-26
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 2
; LENGTH: 543

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-332-175-2

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Query Match      59.2%; Score 1242.5; DB 14; Length 543;
Best Local Similarity 63.5%; Pred. No. 4,8e-113;
Matches 244; Conservative 57; Mismatches 66; Indels 17; Gaps 5;

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QY 2 AADPLDPKSA-----AQNPKRLSFTKPTVLAASRVSDT---TINMKKTKVSTI 50
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 22 AAAPVQPKSATNGQPPAPAPPTPTPRISISSRATVVA-RMEGTSQGGLOTVMKMTVAI 80
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 51 FLVVVLIITGATVFKALEQPHETISORTTIVIOKOTFISCHSCVNSTELDELIOQIVAAI 110
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 81 FVVVVVIVTGVFRLAEQPFESSQKNTIALERAEFLRDHVCSPOLETLIGHALDAD 140
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 111 NAGIIPLGNTSNQISHWDLGSSFFPAGTIVTTTIGFNGISPRTEGKIFCIYALGIPLF 170
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 141 NAGVSPIGNSSNSHMDLGSAFFPAGTIVTTTIGYGNIAPESTEGKIFCIYALGIPLF 200
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 171 GFLLAGVDOLGTTFGKIAKVEDTPIKMNVSQTKIRIISTITIFLPGCVFLPALPAIIF 230
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 201 GFLLAGVDOLGTTFGKISIAVEKVPKQVSQTKIRIVSTILFILAQCTVFYTIYAVIF 260
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 231 KHIEGMSALDAIYFVVVITLTTFGFDYVAGG-SDIEYLDIFYKPVWFWIIVGLAYFAAVL 289
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 261 KYIEGWTALSIYFVVVITLTTFGFDYVAGGAGINVRKYLFWFWIIVGLAYFAAVL 320
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 290 SMIGDMWRVLSKTKKEVEGFRAHAAMTANVTAPEFETRRRLSVEIYDKFORATSI--- 346
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 321 SMIGDMWRVLSKTKKEVEGEIKAHAAEMKANVTAPEFETRRRLSVEIYDKFORATSI--- 380
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 347 -KRLSAELAGNHQELTPCRTL 369
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 381 ERRRLGIDQRAHSLDMLSPKRSV 404
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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RESULT 15
US-10-332-447-10
; Sequence 10, Application US/10332447
; Publication No. US20040053258A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; RAUWANN, Brigitte E.;
; APPLICANT: THORNTON, Michael; DING, Li; YUE, Henry;
; APPLICANT: TANG, Y.Tom; HARLAND, Lee; BUREFORD, Neil;
; APPLICANT: GREENE, Barrie D.; SANTANWALA, Madhu S.;
; APPLICANT: BAUGHN, Mariah R.; YAO, Monique G.; YANG, Junming;
; APPLICANT: ARVIZU, Chandra S.; GANDHI, Aneena R.;
; APPLICANT: HAPFALA, April J.A.; TRIBOULEY, Catherine M.;
; APPLICANT: WALIA, Narinder K.; AU-YOUNG, Janice;
; APPLICANT: WALSH, Roderick T.; RAMKOVAR, Jayalakami;
; APPLICANT: LU, Yan; LU, Dying Aina M.; AZIMZAI, Yalda;
; APPLICANT: LAU, Preeti; ELLIOTT, Vicki S.; NGUYEN, Damien B.;
; APPLICANT: XU, Yunting; SEILHAMER, Jeffrey J.; BOROMSKY, Mark L.;
; APPLICANT: KHAN, Farrah A.; KEARNEY, Liam; THANAVAVLU, Kavitha;
; APPLICANT: DAS, Debopriya; POLICKY, Jennifer L.
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: PI-0149 USN
; CURRENT APPLICATION NUMBER: US/10/332,447
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 60/216,547
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/218,232
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/220,112
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/221,839
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PERL Program
; SEQ ID NO 10
; LENGTH: 724
; TYPE: PRT

```

ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Incycle ID No. US20040053258A1 7472728CD1  
US-10-332-447-10

Query Match 57.9%; Score 1215; DB 12; Length 724;  
Best Local Similarity 62.1%; Pred. No. 3,7e-110;  
Matches 241; Conservative 58; Mismatches 67; Indels 22; Gaps 6;

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QY 2 AAPDLDPKGA-----AONSKPRLSESTKFTVLASRYESDT--TINMKMKTVSTI 50
DB 200 AAPVCOQPKSATNGQPPAPAPPTPTPLRISISSRATVYA-RMEGTSQGLQTVMKMKTVVAI 258
QY 51 FLVVYLILIGATVTFKALBQPHFISORTIVIQOTFISQHSQVNSTEIDELIQIVAAI 110
DB 259 FVVVVVYLVITGVLFRALBQPFESSQNTIALKAEFLRDHVCVSPQELFTLIQHALDAD 318
QY 111 NAGIIPLGNTSNOISHMDLGSFFFAQTVITTTIGFNGNISPRTEGKIFCIIVYALGIPLF 170
DB 319 NAGVSPIGNSSNNSSHMDLGSFAFFFAQTVITTM-YGNIASTEKGKIFCIIVYAFGIPLF 377
QY 171 GFLLAGVGDQGTITFGKIAKVEDTFIKMNVSQTKIRIISTITFIIFGCVLFAALPAITF 230
DB 378 GFLLAGIGDQGTITFGKIAKVEKVRKQVSOQTKIRISTITFIAGCIVFVTLPAVLF 437
QY 231 KHIEGWSALDAIFYVVYITLTITIGFDYVA---GGSDEYLDIFYKPVVWFMLVGLAYF 285
DB 438 KYIEGWTALESIYFVVYITLTITIGFDYVAVVVFRGNAGINRYREMYKPLVWFMLVGLAYF 497
QY 286 AAVLSMTGMDLRYISKKEEVEGEFRAHAEMWTANTAFKETRRLSVEIYDKFORATS 345
DB 498 AAVLSMTGMDLRYLSKKEEVEGEIKAHAAEMKANTAFRETRRLSVEIHDKFORAT 557
QY 346 I---KRLSAELAGNNOELTPCRRTL 369
DB 558 TRSMERRRLGLDQRAHSLDMLSPKRSV 585
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Search completed: July 15, 2004, 18:02:01  
Job time : 48 secs